TABLE III

GENBANK ACCESSION NO:Q9ZSE4 SERINE/THREONINE PROTEIN PHOSPHATASE TYPE 2A.
GENBANK ACCESSION NO:Q16341 PROTEIN-TYROSINE PHOSPHATASE.
GENBANK ACCESSION NO:P2C2_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16) (PP2C).
GENBANK ACCESSION NO:Q92140 PROTEIN PHOSPHATASE 2A, CATALYTIC SUBUNIT, BETA ISOFORM.
GENBANK ACCESSION NO:Q28006 BA14 TYROSINE PHOSPHATASE (EC 3.1.3.48).
GENBANK ACCESSION NO:O14428 SERINE/THREONINE PROTEIN PHOSPHATASE PPT1.
GENBANK ACCESSION NO:P2CG_MOUSE PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (EC 3.1.3.16) (PP2C-GAMMA) (PROTEIN PHOSPHATASE 1C) (FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 13) (FIN13).
GENBANK ACCESSION NO:Q64604 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, F POLYPEPTIDE PRECURSOR (EC 3.1.3.48) (LAR PROTEIN) (LEUKOCYTE ANTIGEN RELATED) (LEUKOCYTE COMMON ANTIGEN-RELATED PHOSPHATASE) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:O43655 PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, R (EC 3.1.3.48) (RECEPTOR PROTEIN TYROSINE PHOSPHATASE) (FRAGMENT).
GENBANK ACCESSION NO:O75551 PROTEIN PHOSPHATASE 2C ALPHA 2.
GENBANK ACCESSION NO:Q64605 LEUKOCYTE COMMON ANTIGEN-RELATED PHOSPHATASE PTP2 PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE LAR-PTP2) (PHOSPHOTYROSINE PHOSPHATASE LAR-PTP2) (PTPASE LAR-PTP2) (PTP NE-3) (PTP-P1) (CPTP1) (PTP-SIGMA).
GENBANK ACCESSION NO:PTPK_HUMAN PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA).
GENBANK ACCESSION NO:PP11_DROME SERINE/THREONINE PROTEIN PHOSPHATASE ALPHA-1 ISOFORM (EC 3.1.3.16).
GENBANK ACCESSION NO:Q42981 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:O88740 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:O81955 PP1A PROTEIN.
GENBANK ACCESSION NO:PTNB_MOUSE PROTEIN-TYROSINE PHOSPHATASE SYP (EC 3.1.3.48).
GENBANK ACCESSION NO:O81956 PP2A1 PROTEIN.
GENBANK ACCESSION NO:P2BA_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, ALPHA ISOFORM) (CAM-PRP CATALYTIC SUBUNIT).
GENBANK ACCESSION NO:P2BA_BOVIN SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, ALPHA ISOFORM) (CAM-PRP CATALYTIC SUBUNIT).
GENBANK ACCESSION NO:PT12_STYPL PROTEIN-TYROSINE PHOSPHATASE 12 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:P2A4_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:PTPM_MOUSE PROTEIN-TYROSINE PHOSPHATASE MU PRECURSOR (EC 3.1.3.48) (R-PTP-MU).
GENBANK ACCESSION NO:PCP2_HUMAN PROTEIN-TYROSINE PHOSPHATASE PCP-2 PRECURSOR (EC 3.1.3.48).
GENBANK ACCESSION NO:P2BC_MOUSE SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, GAMMA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, GAMMA ISOFORM) (CALCINEURIN, TESTIS-SPECIFIC CATALYTIC SUBUNIT) (CAM-PRP CATALYTIC SUBUNIT).
GENBANK ACCESSION NO:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR (EC 3.1.3.48).
GENBANK ACCESSION NO:O61722 PUTATIVE PRENYLATED PROTEIN TYROSINE PHOSPHATASE PRL-1.
GENBANK ACCESSION NO:PPE1_SCHPO SERINE/THREONINE PROTEIN PHOSPHATASE PPE1 (EC 3.1.3.16) (PHOSPHATASE ESP1).
GENBANK ACCESSION NO:Q9XGT7 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:PP14_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 4 (EC 3.1.3.16).
GENBANK ACCESSION NO:O76451 SERINE/THREONINE PROTEIN PHOSPHATASE I (FRAGMENT).
GENBANK ACCESSION NO:O35564 PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, L (EC 3.1.3.48) (FTP-1).
GENBANK ACCESSION NO:PPX1_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 1 (EC 3.1.3.16).

GENBANK ACCESSION NO:O65844 PROTEIN PHOSPHATASE 1, CATALYTIC BETA SUBUNIT.

GENBANK ACCESSION NO:Q62917 LAR RECEPTOR-LINKED TYROSINE PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:O65845 PROTEIN PHOSPHATASE 1, CATALYTIC GSMMS SUBUNIT.

GENBANK ACCESSION NO:Q64538 PHOSPHOPROTEIN PHOSPHATASE (FRAGMENT).

GENBANK ACCESSION NO:O65846 PROTEIN PHOSPHATASE 1 CATALITIC SUBUNIT.

GENBANK ACCESSION NO:PTN3_HUMAN PROTEIN-TYROSINE PHOSPHATASE H1 (EC 3.1.3.48) (PTP-H1).

GENBANK ACCESSION NO:P2C3_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG 3 (EC 3.1.3.16) (PP2C-3).

GENBANK ACCESSION NO:O65847 PROTEIN PHOSPHATASE 1, CATALYTIC EPSILON SUBUNIT.

GENBANK ACCESSION NO:PPP6_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 6 (EC 3.1.3.16) (PP6).

GENBANK ACCESSION NO:O88591 PROTEIN PHOSPHATASE TYPE 2A CATALYTIC SUBUNIT ALPHA ISOFORM.

GENBANK ACCESSION NO:P2AB_PIG SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16) (FRAGMENT).

GENBANK ACCESSION NO:PTO6_STYPL PROTEIN-TYROSINE PHOSPHATASE 6 (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:P2A_BRANA SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT (EC 3.1.3.16) (FRAGMENT).

GENBANK ACCESSION NO:P2A_MEDSA SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT (EC 3.1.3.16).

GENBANK ACCESSION NO:PTNC_HUMAN PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1).

GENBANK ACCESSION NO:O15253 SERINE /THREONINE PROTEIN PHOSPHATASE.

GENBANK ACCESSION NO:P2CB_MOUSE PROTEIN PHOSPHATASE 2C BETA ISOFORM (EC 3.1.3.16) (PP2C-BETA) (IA) (PROTEIN PHOSPHATASE 1B).

GENBANK ACCESSION NO:Q61152 PROTEIN-TYROSINE PHOSPHATASE 18 (EC 3.1.3.48) (PTP-K1) (FETAL LIVER PHOSPHATASE 1) (FLP1) (PTP 49) (PTP HSCF).

GENBANK ACCESSION NO:O22626 PROTEIN PHOSPHATASE X ISOFORM 2.

GENBANK ACCESSION NO:Q9XGU3 PHOSPHATASE PP1.

GENBANK ACCESSION NO:PTPF_HUMAN LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) (EC 3.1.3.48).

GENBANK ACCESSION NO:Q64621 RECEPTOR-LINKED PROTEIN TYROSINE PHOSPHATASE (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).

GENBANK ACCESSION NO:YME1_CAEEL PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE F56C9.1 IN CHROMOSOME III (EC 3.1.3.16).

GENBANK ACCESSION NO:Q64622 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).

GENBANK ACCESSION NO:Q24708 PROTEIN-TYROSINE PHOSPHATASE CORKSCREW (EC 3.1.3.48) (CSW) (FRAGMENT).

GENBANK ACCESSION NO:Q15718 PTPSIGMA PRECURSOR (EC 3.1.3.48).

GENBANK ACCESSION NO:PTPA_RAT PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURSOR (EC 3.1.3.48) (R-PTP- ALPHA).

GENBANK ACCESSION NO:Q63739 TYROSINE PHOSPHATASE.

GENBANK ACCESSION NO:P91569 PROBABLE SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).

GENBANK ACCESSION NO:WZB_ECOLI PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE WZB (EC 3.1.3.48).

GENBANK ACCESSION NO:PP1G_MOUSE SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1G).

GENBANK ACCESSION NO:O88765 PROTEIN TYROSINE PHOSPHATASE.

GENBANK ACCESSION NO:Q98945 PROTEIN TYROSINE PHOSPHATASE CRYP-2 PRECURSOR (EC 3.1.3.48).

GENBANK ACCESSION NO:YOR5_KLEPN PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (ORF5).

GENBANK ACCESSION NO:P2BB_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, BETA ISOFORM) (CAM-PRP CATALYTIC SUBUNIT).

GENBANK ACCESSION NO:Q9Y0B7 PROTEIN PHOSPHATASE 4 CATALYTIC SUBUNIT.

GENBANK ACCESSION NO:Q04071 PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT C (EC 3..3.16) (PP-2BC) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT) (FRAGMENT).

GENBANK ACCESSION NO:YWLE_BACSU PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:Q92TF1 PUTATIVE TRANSCRIPTION FACTOR (FRAGMENT).

GENBANK ACCESSION NO:Q62132 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, Q PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE SL) (PHOSPHOTYROSINE PHOSPHATASE).

GENBANK ACCESSION NO:P70602 PROTEIN TYROSINE PHOSPHATASE 20 (EC 3.1.3.48).

GENBANK ACCESSION NO:P2A1_NEUCR SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT (EC 3.1.3.16).

GENBANK ACCESSION NO:Q62135 PROTEIN-TYROSINE PHOSPHATASE 13 (EC 3.1.3.48) (RIP).

GENBANK ACCESSION NO:O17047 PROTEIN PHOSPHATASE WITH EF-HANDS.

GENBANK ACCESSION NO:O43049 SERINE/THREONINE PROTEIN PHOSPHATASE.

GENBANK ACCESSION NO:Q9XF94 SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALYTIC SUBUNIT.

GENBANK ACCESSION NO:PPP4_RABIT SERINE/THREONINE PROTEIN PHOSPHATASE 4 (EC 3.1.3.16) (PP4) (PROTEIN PHOSPHATASE X) (PP-X).

GENBANK ACCESSION NO:PPZ_SCHPO SERINE/THREONINE PROTEIN PHOSPHATASE PP-Z (EC 3.1.3.16).

GENBANK ACCESSION NO:Q12974 PROTEIN-TYROSINE PHOSPHATASE.

GENBANK ACCESSION NO:Q63745 PROTEIN TYROSINE PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:P2A3_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PPH3 (EC 3.1.3.16).

GENBANK ACCESSION NO:P97470 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16) (FRAGMENT).

GENBANK ACCESSION NO:O75664 DJ707K17.1 (RECEPTOR PROTEIN TYROSINE PHOSPHATASE (RPTP-RHO, EC 3.1.3.48)) (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:Q62937 PP-1M (FRAGMENT).

GENBANK ACCESSION NO:Q27786 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).

GENBANK ACCESSION NO:Q27787 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).

GENBANK ACCESSION NO:PTN6_HUMAN PROTEIN-TYROSINE PHOSPHATASE 1C (EC 3.1.3.48) (PTP-1C) (HEMATOPOIETIC CELL PROTEIN PHOSPHATASE) (SH-PTP1).

GENBANK ACCESSION NO:Q60998 PROTEIN-TYROSINE PHOSPHATE PHI (EC 3.1.3.48) (PTP PHI).

GENBANK ACCESSION NO:PTPA_MYCTU PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PTPASE).

GENBANK ACCESSION NO:PT09_STYPL PROTEIN-TYROSINE PHOSPHATASE 9 (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:Q99849 PROTEIN TYROSINE PHOSPHATASE HOMOLOG HPRL-R (FRAGMENT).

GENBANK ACCESSION NO:P2C_LEISH PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C).

GENBANK ACCESSION NO:P2CA_RAT PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) (PROTEIN PHOSPHATASE 1A).

GENBANK ACCESSION NO:PTPA_HUMAN PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURSOR (EC 3.1.3.48) (R-PTP- ALPHA).

GENBANK ACCESSION NO:P2A1_SCHPO MINOR SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC SUBUNIT (EC 3.1.3.16).

GENBANK ACCESSION NO:PTN8_MOUSE HEMATOPOIETIC CELL PROTEIN-TYROSINE PHOSPHATASE 70Z-PEP (EC 3.1.3.48).

GENBANK ACCESSION NO:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT).

GENBANK ACCESSION NO:Q9YDZ2 266AA LONG HYPOTHETICAL SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT.

GENBANK ACCESSION NO:Q10729 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M21 SUBUNIT (21 KDA SUBUNIT).

GENBANK ACCESSION NO:PP1_BRANA SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC 3.1.3.16) (FRAGMENT).

GENBANK ACCESSION NO:Q64641 BRAIN-ENRICHED MEMBRANE-ASSOCIATED PROTEIN TYROSINE PHOSPHATASE (BEM)-1 (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:Q64642 BRAIN-ENRICHED MEMBRANE-ASSOCIATED PROTEIN TYROSINE PHOSPHATASE 2 (EC 3.1.3.48) (BEM-2) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).

GENBANK ACCESSION NO:P2B2_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT A2 (EC 3.1.3.16) (CALCINEURIN A2) (CALMODULIN-BINDING PROTEIN 2).

GENBANK ACCESSION NO:O77294 SERINE-THREONINE PROTEIN PHOSPHATASE.

GENBANK ACCESSION NO:Q64486 MPTPDELTA (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).

GENBANK ACCESSION NO:PP11_SCHPO SERINE/THREONINE PROTEIN PHOSPHATASE PP1-1 (EC 3.1.3.16).

GENBANK ACCESSION NO:Q64487 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, D PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE DELTA) (R-PTP-DELTA).

GENBANK ACCESSION NO:PT10_STYPL PROTEIN-TYROSINE PHOSPHATASE 10 (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:EPSP_BURSO PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE EPSP (EC 3.1.3.48).

GENBANK ACCESSION NO:P2A2_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALYTIC SUBUNIT (EC 3.1.3.16).

GENBANK ACCESSION NO:PTPK_MOUSE PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA).

GENBANK ACCESSION NO:Q9XGH7 PROTEIN PHOSPHATASE 2A CATALYTIC SUBUNIT (EC 3.1.3.16).

GENBANK ACCESSION NO:Q00219 SERINE/THREONINE PROTEIN PHOSPHATASE PP1(5.9) (EC 3.1.3.16).

GENBANK ACCESSION NO:P2BA_MOUSE SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, ALPHA ISOFORM) (CAM-PRP CATALYTIC SUBUNIT).

GENBANK ACCESSION NO:PP12_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2 (EC 3.1.3.16).

GENBANK ACCESSION NO:O43941 PROTEIN PHOSPHATASE-2C.

GENBANK ACCESSION NO:LAR_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN- TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).

GENBANK ACCESSION NO:P2CA_RABIT PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (PROTEIN PHOSPHATASE 1A) (IA).

GENBANK ACCESSION NO:Q07808 PROTEIN-TYROSINE PHOSPHATASE 1 (EC 3.1.3.48) (PTPASE 1) (PTP-P1).

GENBANK ACCESSION NO:Q90815 PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:P2A_DROME SERINE/THREONINE PROTEIN PHOSPHATASE PP2A (EC 3.1.3.16) (MICROTUBULE STAR PROTEIN).

GENBANK ACCESSION NO:Q24495 RECEPTOR PROTEIN-TYROSINE PHOSPHATASE PRECURSOR (EC 3.1.3.48).

GENBANK ACCESSION NO:Q90816 PROTEIN-TYROSINE PHOSPHATASE (FRAGMENT).

GENBANK ACCESSION NO:Q64653 PROTEIN TYROSINE PHOSPHATASE (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).

GENBANK ACCESSION NO:O63682 PROTEIN PHOSPHATASE-1A (FRAGMENT).

GENBANK ACCESSION NO:Y328_SYNY3 PUTATIVE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:PPP4_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 4 (EC 3.1.3.16) (PP4) (PROTEIN PHOSPHATASE X) (PP-X).

GENBANK ACCESSION NO:YQF3_CAEEL PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C34C12.3 IN CHROMOSOME III (EC 3.1.3.16).

GENBANK ACCESSION NO:Q64494 PROTEIN-TYROSINE PHOSPHATASE S (EC 3.1.3.48) (R-PTP-S) (FRAGMENT).

GENBANK ACCESSION NO:Q64495 PROTEIN-TYROSINE PHOSPHATASE DELTA (EC 3.1.3.48) (R-PTP-DELTA) (FRAGMENT).

GENBANK ACCESSION NO:Q29585 PHOSPHOPROTEIN PHOSPHATASE (EC 3.1.3.16) (SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE) (PROTEIN PHOSPHATASE-1) (PROTEIN PHOSPHATASE-2A) (PROTEIN PHOSPHATASE-2B) (PROTEIN PHOSPHATASE-2C) (FRAGMENT).

GENBANK ACCESSION NO:Q64497 PROTEIN-TYROSINE PHOSPHATASE BETA (EC 3.1.3.48) (R-PTP- BETA) (FRAGMENT).

GENBANK ACCESSION NO:PP1_BRAOL SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC 3.1.3.16).

GENBANK ACCESSION NO:Q62797 PROTEIN TYROSINE PHOSPHATASE BK PRECURSOR (EC 3.1.3.48) (PTP-BK) (PROTEIN TYROSINE PHOSPHATASE D30).

GENBANK ACCESSION NO:O75688 PP2C PROTEIN.

GENBANK ACCESSION NO:PT04_STYPL PROTEIN-TYROSINE PHOSPHATASE 4 (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:Q13332 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, S PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE SIGMA) (R-PTP-SIGMA) (PTPRS).

GENBANK ACCESSION NO:YT91_CAEEL PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C06A1.3 IN CHROMOSOME II (EC 3.1.3.16).

GENBANK ACCESSION NO:PTPD_HUMAN PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (EC 3.1.3.48) (R-PTP- DELTA).

GENBANK ACCESSION NO:O22662 PROTEIN PHOSPHATASE U (FRAGMENT).

GENBANK ACCESSION NO:O15297 WIP1.

GENBANK ACCESSION NO:PP12_DROME SERINE/THREONINE PROTEIN PHOSPHATASE ALPHA-2 ISOFORM (EC 3.1.3.16).
GENBANK ACCESSION NO:O62829 PROTEIN PHOSPHATASE 2C ALPHA (EC 3.1.3.16).
GENBANK ACCESSION NO:Q93095 PROTEIN TYROSINE PHOSPHATASE PEP (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).
GENBANK ACCESSION NO:Q91556 PROTEIN TYROSINE PHOSPHATASE ALPHA PRECURSOR (EC 3.1.3.48).
GENBANK ACCESSION NO:O52787 PTP PROTEIN.
GENBANK ACCESSION NO:Q93096 PROTEIN TYROSINE PHOSPHATASE HPRL-1N (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).
GENBANK ACCESSION NO:PTNC_MOUSE PROTEIN-TYROSINE PHOSPHATASE P19 (EC 3.1.3.48) (P19-PTP) (MPTP-PEST).
GENBANK ACCESSION NO:Q62884 DENSITY-ENHANCED PHOSPHATASE-1 PRECURSOR (EC 3.1.3.48) (DEP-1) (VASCULAR PROTEIN TYROSINE PHOSPHATASE 1).
GENBANK ACCESSION NO:P2BB_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, BETA ISOFORM) (CAM-PRP CATALYTIC SUBUNIT).
GENBANK ACCESSION NO:PPAC_BOVIN LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (EC 3.1.3.48) (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (EC 3.1.3.2) (PTPASE).
GENBANK ACCESSION NO:Q99952 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:Q9YHE4 PROTEIN TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q9YHE5 PROTEIN TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q9YHE6 PROTEIN TYROSINE PHOSPHATASE SH-PTP2 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q9YHE7 PROTEIN TYROSINE PHOSPHATASE H1 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:O00810 PROTEIN TYROSINE PHOSPHATASE.
GENBANK ACCESSION NO:PP1B_DROME SERINE/THREONINE PROTEIN PHOSPHATASE BETA ISOFORM (EC 3.1.3.16).
GENBANK ACCESSION NO:PPAC_RAT LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE ACP1/ACP2 (EC 3.1.3.48) (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (EC 3.1.3.2) (PTPASE).
GENBANK ACCESSION NO:P2B1_DROME SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT 1 (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A1 SUBUNIT).
GENBANK ACCESSION NO:PPV_DROME SERINE/THREONINE PROTEIN PHOSPHATASE PP-V (EC 3.1.3.16).
GENBANK ACCESSION NO:Q24032 CORKSCREW PROTEIN Y1229 (EC 3.1.3.48).
GENBANK ACCESSION NO:Q24033 PROTEIN-TYROSINE PHOSPHATASE CORKSCREW, ISOFORM 4A (EC 3.1.3.48) (CSW).
GENBANK ACCESSION NO:Q42812 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:O62830 PROTEIN PHOSPHATASE 2C BETA (EC 3.1.3.16).
GENBANK ACCESSION NO:Q95040 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:PP1_PHAVU SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC 3.1.3.16).
GENBANK ACCESSION NO:P70643 RECEPTOR TYPE PROTEIN TYROSINE PHOPHATASE PSI (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:PP15_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 5 (EC 3.1.3.16).
GENBANK ACCESSION NO:P70644 RECEPTOR TYPE PROTEIN TYROSINE PHOSPHATASE MY (FRAGMENT).
GENBANK ACCESSION NO:O18931 PROTEIN PHOSPHATASE TYPE 1 BETA CATALYTIC SUBUNIT (FRAGMENT).
GENBANK ACCESSION NO:O04856 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:O18932 PROTEIN PHOSPHATASE 2A-ALPHA CATALYTIC SUBUNIT (FRAGMENT).
GENBANK ACCESSION NO:O04857 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:O04858 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:PPX2_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2 (EC 3.1.3.16).
GENBANK ACCESSION NO:P2A1_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1

CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:O04859 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:Q9Y2R2 PROTEIN TYROSINE PHOSPHATASE HOMOLOG (EC 3.1.3.48).
GENBANK ACCESSION NO:Q9WU22 PROTEIN TYROSINE PHOSPHATASE MEG-01 (EC 3.1.3.48).
GENBANK ACCESSION NO:O43966 PROTEIN PHOSPHATASE 2C.
GENBANK ACCESSION NO:PP1_MEDVA SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC 3.1.3.16).
GENBANK ACCESSION NO:Q64675 LEUKOCYTE COMMON ANTIGEN-RELATED PHOSPHATASE PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:PTN4_HUMAN PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (PTPASE-MEG1) (MEG).
GENBANK ACCESSION NO:P2CA_HUMAN PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) (PROTEIN PHOSPHATASE 1A).
GENBANK ACCESSION NO:P2AA_CHICK SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-ALPHA, CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:PT07_STYPL PROTEIN-TYROSINE PHOSPHATASE 7 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:PP11_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP1-1 (EC 3.1.3.16).
GENBANK ACCESSION NO:PPAL_SCHPO LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (EC 3.1.3.48) (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (EC 3.1.3.2) (PTPASE) (SMALL TYROSINE PHOSPHATASE).
GENBANK ACCESSION NO:Q9Y879 CALCINEURIN A CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:P2CB_RAT PROTEIN PHOSPHATASE 2C BETA ISOFORM (EC 3.1.3.16) (PP2C-BETA) (IA) (PROTEIN PHOSPHATASE 1B).
GENBANK ACCESSION NO:O15712 PROTEIN PHOSPHATASE 2B.
GENBANK ACCESSION NO:PPZ1_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP-Z1 (EC 3.1.3.16).
GENBANK ACCESSION NO:Q9X4B8 PUTATIVE ACID PHOSPHATASE WZB.
GENBANK ACCESSION NO:PTN6_MOUSE PROTEIN-TYROSINE PHOSPHATASE 1C (EC 3.1.3.48) (PTP-1C) (HEMATOPOIETIC CELL PROTEIN-TYROSINE PHOSPHATASE) (70Z-SHP) (SH-PTP1).
GENBANK ACCESSION NO:O04860 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:P2C2_SCHPO PROTEIN PHOSPHATASE 2C HOMOLOG 2 (EC 3.1.3.16) (PP2C-2).
GENBANK ACCESSION NO:P2B1_CRYNE SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT A1 (EC 3.1.3.16) (CALCINEURIN A1).
GENBANK ACCESSION NO:Q64046 MG2+ DEPENDENT PROTEIN PHOSPHATASE BETA ISOFORM.
GENBANK ACCESSION NO:Q61373 PROTEIN TYROSINE PHOSPHATASE (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q9X2E5 PROTEIN PHOSPHATASE 2A CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:O81716 PROTEIN PHOSPHATASE 2C - LIKE PROTEIN.
GENBANK ACCESSION NO:O14829 PROTEIN PHOSPHATASE WITH EF-HANDS-1.
GENBANK ACCESSION NO:Q16826 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:PP11_ACECL SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1 (EC 3.1.3.16).
GENBANK ACCESSION NO:Q16827 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, O PRECURSOR (EC 3.1.3.48) (PROTEIN TYROSINE PHOSPHATASE U2) (GLOMERULAR EPITHELIAL PROTEIN 1) (GLEPP1) (PHOSPHOTYROSINE PHOSPHATASE U2) (PTPASE U2) (PTP-U2).
GENBANK ACCESSION NO:O75870 PTPSIGMA (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:PTPA_MOUSE PROTEIN-TYROSINE PHOSPHATASE ALPHA PRECURSOR (EC 3.1.3.48) (R-PTP- ALPHA) (LCA-RELATED PHOSPHATASE).
GENBANK ACCESSION NO:O43979 SERINE-THREONINE PHOSPHOPROTEIN PHOSPHATASE.
GENBANK ACCESSION NO:O94748 PROTEIN PHOSPHATASE-Z-LIKE SERINE/THREONINE PROTEIN PHOSPHATASE.
GENBANK ACCESSION NO:Q90687 PROTEIN-TYROSINE PHOSPHATASE N11 (EC 3.1.3.48) (PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 11).
GENBANK ACCESSION NO:PTP6_DROME PROTEIN-TYROSINE PHOSPHATASE DPTP PRECURSOR (EC 3.1.3.48) (PROTEIN- TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).
GENBANK ACCESSION NO:Q62987 PROTEIN TYROSINE PHOSPHATASE SH-PTP2 (FRAGMENT).
GENBANK ACCESSION NO:Q62988 PROTEIN TYROSINE PHOSPHATASE ALPHA (FRAGMENT).
GENBANK ACCESSION NO:Q62989 PROTEIN TYROSINE PHOSPHATASE GAMMA (FRAGMENT).
GENBANK ACCESSION NO:AMSI_ERWAM PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE AMSI (EC 3.1.3.48).
GENBANK ACCESSION NO:PT16_STYPL PROTEIN-TYROSINE PHOSPHATASE 16 (EC 3.1.3.48)

(FRAGMENT).

GENBANK ACCESSION NO:PPQ1_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PPQ (EC 3.1.3.16).

GENBANK ACCESSION NO:PPY_DROME SERINE/THREONINE PROTEIN PHOSPHATASE PP-Y (EC 3.1.3.16).

GENBANK ACCESSION NO:O14830 PROTEIN PHOSPHATASE WITH EF-HANDS-2 LONG FORM.

GENBANK ACCESSION NO:O14831 PROTEIN PHOSPHATASE WITH EF-HANDS-2 SHORT FORM.

GENBANK ACCESSION NO:O04951 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).

GENBANK ACCESSION NO:O77023 DPP2C1.

GENBANK ACCESSION NO:Q42912 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).

GENBANK ACCESSION NO:RDGC_DROME SERINE/THREONINE PROTEIN PHOSPHATASE RDGC (EC 3.1.3.16) (RETINAL DEGENERATION C PROTEIN).

GENBANK ACCESSION NO:O76932 SERINE /THREONINE SPECIFIC PROTEIN PHOSPHATASE 4 (EC 3.1.3.16).

GENBANK ACCESSION NO:P2AA_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-ALPHA, CATALYTIC SUBUNIT (EC 3.1.3.16) (REPLICATION PROTEIN C) (RP-C).

GENBANK ACCESSION NO:P2A4_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-LIKE PPG1 (EC 3.1.3.16).

GENBANK ACCESSION NO:Q9W6R4 PROTEIN PHOSPHATASE 1.

GENBANK ACCESSION NO:PP1_EMENI SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC 3.1.3.16).

GENBANK ACCESSION NO:O59927 SERINE/THREONINE PROTEIN PHOSPHATASE TYPE 1.

GENBANK ACCESSION NO:PTPA_STRCO LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PTPASE) (SMALL, ACIDIC PHOSPHOTYROSINE PROTEIN PHOSPHATASE) (PY PROTEIN PHOSPHATASE).

GENBANK ACCESSION NO:Q64696 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, F POLYPEPTIDE (EC 3.1.3.48) (LAR PROTEIN) (LEUKOCYTE ANTIGEN RELATED) (FRAGMENT).

GENBANK ACCESSION NO:PTN7_HUMAN PROTEIN-TYROSINE PHOSPHATASE LC-PTP (EC 3.1.3.48) (HEMATOPOIETIC PROTEIN-TYROSINE PHOSPHATASE) (HEPTP).

GENBANK ACCESSION NO:CSW_DROME PROTEIN-TYROSINE PHOSPHATASE CORKSCREW (EC 3.1.3.48).

GENBANK ACCESSION NO:Q64699 PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, S PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE SIGMA) (RPTP-SIGMA) (PROTEIN TYROSINE PHOSPHATASE PTPT9) (PTPASE NU-3).

GENBANK ACCESSION NO:PP11_TRYBB SERINE/THREONINE PROTEIN PHOSPHATASE PP1(4.8) (EC 3.1.3.16).

GENBANK ACCESSION NO:PP1_MAIZE SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC 3.1.3.16).

GENBANK ACCESSION NO:PT25_STYPL PROTEIN-TYROSINE PHOSPHATASE 25 (EC 3.1.3.48) (FRAGMENT).

GENBANK ACCESSION NO:PP1A_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1A).

GENBANK ACCESSION NO:PPP5_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT).

GENBANK ACCESSION NO:PTPB_HUMAN PROTEIN-TYROSINE PHOSPHATASE BETA PRECURSOR (EC 3.1.3.48) (R-PTP- BETA).

GENBANK ACCESSION NO:P2C1_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C F42G9.1 (EC 3.1.3.16) (PP2C).

GENBANK ACCESSION NO:P2A2_SCHPO MAJOR SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALYTIC SUBUNIT (EC 3.1.3.16).

GENBANK ACCESSION NO:O44328 RECEPTOR TYROSINE PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:O94044 PHOSPHOTYROSINE PROTEIN PHOSPHATASE.

GENBANK ACCESSION NO:O44329 RECEPTOR TYROSINE PHOSPHATASE (EC 3.1.3.48).

GENBANK ACCESSION NO:PTPJ_HUMAN PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.1.3.48) (R-PTP-ETA) (DENSITY ENHANCED PHOSPHATASE-1) (DEP-1) (CD148 ANTIGEN).

GENBANK ACCESSION NO:Q9YI74 SERINE/THREONINE PHOSPHATASE.

GENBANK ACCESSION NO:O08367 SERINE /THREONINE SPECIFIC PROTEIN PHOSPHATASE (EC 3.1.3.16) (SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE) (PHOSPHOPROTEIN PHOSPHATASE) (PROTEIN PHOSPHATASE-1) (PROTEIN PHOSPHATASE-2A) (PROTEIN PHOSPHATASE-2B) (PROTEIN PHOSPHATASE-2C).

GENBANK ACCESSION NO:Q9YI75 SERINE/THREONINE PHOSPHATASE.

GENBANK ACCESSION NO:Q9YI76 SERINE/THREONINE PHOSPHATASE.

GENBANK ACCESSION NO:O57438 CALCINEURIN A.

GENBANK ACCESSION NO:PTP1_DROME PROTEIN-TYROSINE PHOSPHATASE 10D PRECURSOR (EC 3.1.3.48) (RECEPTOR- LINKED PROTEIN-TYROSINE PHOSPHATASE 10D).

GENBANK ACCESSION NO:O82469 PROTEIN PHOSPHATASE-2C.

GENBANK ACCESSION NO:PP12_SCHPO SERINE/THREONINE PROTEIN PHOSPHATASE PP1-2 (EC 3.1.3.16) (SUPPRESSOR PROTEIN SDS21).
GENBANK ACCESSION NO:PT11_STYPL PROTEIN-TYROSINE PHOSPHATASE 11 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:PTP9_DROME PROTEIN-TYROSINE PHOSPHATASE 99A PRECURSOR (EC 3.1.3.48) (RECEPTOR- LINKED PROTEIN-TYROSINE PHOSPHATASE 99A).
GENBANK ACCESSION NO:Q9Y1W9 SPTPN6 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:P2A3_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:PTPO_RAT OSTEOTESTICULAR PROTEIN TYROSINE PHOSPHATASE PRECURSOR (EC 3.1.3.48) (OST-PTP).
GENBANK ACCESSION NO:P2BB_MOUSE SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, BETA ISOFORM) (CAM-PRP CATALYTIC SUBUNIT) (FRAGMENT).
GENBANK ACCESSION NO:Q14513 TYROSINE PHOSPHATASE PRECURSOR (EC 3.1.3.48).
GENBANK ACCESSION NO:PP1G_XENLA SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1G).
GENBANK ACCESSION NO:P70125 PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, L (EC 3.1.3.48) (RECEPTOR PROTEIN TYROSINE PHOSPHATASE-LAMDA).
GENBANK ACCESSION NO:P2B1_SCHPO SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:Q23345 SIMILAR TO OTHER PROTEIN PHOSPHATASES 1.
GENBANK ACCESSION NO:PPAL_YEAST LOW MOLECULAR WEIGHT PHOSPHOTYROSINE PROTEIN PHOSPHATASE (EC 3.1.3.48) (LOW MOLECULAR WEIGHT CYTOSOLIC ACID PHOSPHATASE) (EC 3.1.3.2) (PTPASE).
GENBANK ACCESSION NO:PP13_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 3 (EC 3.1.3.16).
GENBANK ACCESSION NO:O82470 PROTEIN PHOSPHATASE-2C.
GENBANK ACCESSION NO:O82471 PROTEIN PHOSPHATASE-2C.
GENBANK ACCESSION NO:O49346 A SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16) (SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE) (PHOSPHOPROTEIN PHOSPHATASE) (PROTEIN PHOSPHATASE-1) (PROTEIN PHOSPHATASE-2A) (PROTEIN PHOSPHATASE-2B) (PROTEIN PHOSPHATASE-2C).
GENBANK ACCESSION NO:YSD1_CAEEL PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C23G10.1 IN CHROMOSOME II (EC 3.1.3.16).
GENBANK ACCESSION NO:PTN2_HUMAN T-CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP).
GENBANK ACCESSION NO:P2C2_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG 2 (EC 3.1.3.16) (PP2C-2).
GENBANK ACCESSION NO:PPP5_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT).
GENBANK ACCESSION NO:O82479 PROTEIN PHOSPHATASE-2C (FRAGMENT).
GENBANK ACCESSION NO:P2C_PARTE PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C).
GENBANK ACCESSION NO:Q9Y1X5 SPTPR2B (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q9Y1X6 SPTPR4 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:P2CG_HUMAN PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (EC 3.1.3.16) (PP2C-GAMMA) (PROTEIN PHOSPHATASE 1C).
GENBANK ACCESSION NO:P2CG_BOVIN PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (EC 3.1.3.16) (PP2C-GAMMA) (PROTEIN PHOSPHATASE 1B) (MAGNESIUM-DEPENDENT CALCIUM INHIBITABLE PHOSPHATASE) (MCPP).
GENBANK ACCESSION NO:P2A_HELAN SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:PTNB_HUMAN PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH-PTP3) (SH-PTP2) (SHP-2).
GENBANK ACCESSION NO:P2CA_MOUSE PROTEIN PHOSPHATASE 2C ALPHA ISOFORM (EC 3.1.3.16) (PP2C-ALPHA) (IA) (PROTEIN PHOSPHATASE 1A).
GENBANK ACCESSION NO:P91420 PROBABLE SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:PTPE_HUMAN PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).
GENBANK ACCESSION NO:Q15255 PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC 3.1.3.48) (R-PTP-ETA).
GENBANK ACCESSION NO:Q91054 CD45 HOMOLOG (EC 3.1.3.48).
GENBANK ACCESSION NO:Q15256 PROTEIN-TYROSINE PHOSPHATASE PCPTP1 PRECURSOR (EC 3.1.3.48) (PROTEIN- TYROSINE-PHOSPHATASE PCPTP1) (NC-PTPCOM1).
GENBANK ACCESSION NO:SD22_SCHPO PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT

SDS22.
GENBANK ACCESSION NO:O15757 PROTEIN PHOSPHATASE TYPE 1-LIKE CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:PTPM_HUMAN PROTEIN-TYROSINE PHOSPHATASE MU PRECURSOR (EC 3.1.3.48) (R-PTP-MU).
GENBANK ACCESSION NO:PP13_DROME SERINE/THREONINE PROTEIN PHOSPHATASE ALPHA-3 ISOFORM (EC 3.1.3.16).
GENBANK ACCESSION NO:Q27475 PROBABLE SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:PTNB_RAT PROTEIN-TYROSINE PHOSPHATASE SYP (EC 3.1.3.48).
GENBANK ACCESSION NO:P2BC_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, GAMMA ISOFORM (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT, GAMMA ISOFORM) (CALCINEURIN, TESTIS-SPECIFIC CATALYTIC SUBUNIT) (CAM-PRP CATALYTIC SUBUNIT).
GENBANK ACCESSION NO:Q95097 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:Q9ZSQ7 PROTEIN PHOSPHATASE 2C HOMOLOG.
GENBANK ACCESSION NO:YD44_SCHPO PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C22H10.04 (EC 3.1.3.16).
GENBANK ACCESSION NO:Q9WUV7 SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:PPX1_PARTE SERINE/THREONINE PROTEIN PHOSPHATASE PP-X HOMOLOG (EC 3.1.3.16).
GENBANK ACCESSION NO:PTPO_MOUSE EMBRYONIC STEM CELL PROTEIN TYROSINE PHOSPHATASE PRECURSOR (EC 3.1.3.48) (ES CELL PHOSPHATASE).
GENBANK ACCESSION NO:P2B2_DROME SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT 2, (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A2 SUBUNIT).
GENBANK ACCESSION NO:Q9Z1G2 SERINE/THREONINE PROTEIN PHOSPHATASE TYPE 1 ALPHA.
GENBANK ACCESSION NO:Q07161 PROTEIN PHOSPHATASE PP1-ALPHA 2, CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:O15920 PROTEIN PHOSPHATASE-BETA.
GENBANK ACCESSION NO:P2B_EMENI SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT).
GENBANK ACCESSION NO:YY06_CAEEL PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C27B7.6 IN CHROMOSOME IV (EC 3.1.3.16).
GENBANK ACCESSION NO:Q29500 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:Q15263 PROTEIN TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1).
GENBANK ACCESSION NO:Q15264 PROTEIN TYROSINE PHOSPHATASE (PTP-BAS, TYPE 2).
GENBANK ACCESSION NO:Q15426 PROTEIN-TYROSINE-PHOSPHATASE, RECEPTOR-TYPE, H PRECURSOR (EC 3.1.3.48) (PROTEIN TYROSINE PHOSPHATASE SAP-1) (STOMACH CANCER-ASSOCIATED PTP).
GENBANK ACCESSION NO:PP12_RABIT SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 2 CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1A).
GENBANK ACCESSION NO:O02658 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:Q15265 PROTEIN TYROSINE PHOSPHATASE (PTP-BAS, TYPE 3).
GENBANK ACCESSION NO:O70275 PROTEIN TYROSINE PHOSPHATASE 4A3 (MPRL-3).
GENBANK ACCESSION NO:Q27560 SERINE/THREONINE PROTEIN PHOSPHATASE CALCINEURIN A (EC 3.1.3.16).
GENBANK ACCESSION NO:082733 SERINE/THREONINE PROTEIN PHOSPHATASE TYPE ONE.
GENBANK ACCESSION NO:P2AB_RABIT SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:PP16_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 6 (EC 3.1.3.16).
GENBANK ACCESSION NO:F91273 PROBABLE SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:082734 SERINE/THREONINE PROTEIN PHOSPHATASE TYPE ONE.
GENBANK ACCESSION NO:O75365 HPRL-3.
GENBANK ACCESSION NO:P81718 PROTEIN-TYROSINE PHOSPHATASE N6 (EC 3.1.3.48).
GENBANK ACCESSION NO:P2A_ACECL SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:P2A2_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-2 CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:Q9W6V5 SUPPORTING-CELL ANTIGEN PRECURSOR (EC 3.1.3.48).
GENBANK ACCESSION NO:Q04101 PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (FRAGMENT).
GENBANK ACCESSION NO:PP12_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP1-2 (EC

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3.1.3.16).
GENBANK ACCESSION NO:Q04102 PROTEIN PHOSPHATASE PP1-C CATALYTIC SUBUNIT (EC
3.1.3.16) (FRAGMENT).
GENBANK ACCESSION NO:Q04103 PROTEIN PHOSPHATASE PP1-D CATALYTIC SUBUNIT (EC
3.1.3.16) (FRAGMENT).
GENBANK ACCESSION NO:PPT1_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE T (EC
3.1.3.16) (PPT).
GENBANK ACCESSION NO:Q04104 PROTEIN PHOSPHATASE PP-X CATALYTIC SUBUNIT (EC
3.1.3.16) (FRAGMENT).
GENBANK ACCESSION NO:P2AA_MOUSE SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-ALPHA,
CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:PPP6_RAT SERINE/THREONINE PROTEIN PHOSPHATASE 6 (EC
3.1.3.16) (PP6) (PROTEIN PHOSPHATASE V) (PP-V).
GENBANK ACCESSION NO:PP1G_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA
CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1G).
GENBANK ACCESSION NO:PPZ2_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE PP-Z2 (EC
3.1.3.16).
GENBANK ACCESSION NO:Q64501 PROTEIN TYROSINE PHOSPHATASE D28 (EC 3.1.3.48)
(PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE)
(FRAGMENT).
GENBANK ACCESSION NO:Q64502 PROTEIN TYROSINE PHOSPHATASE (EC 3.1.3.48) (PROTEIN-
TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).
GENBANK ACCESSION NO:Q12923 PROTEIN-TYROSINE PHOSPHATASE, NONRECEPTOR-TYPE, 13
(EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE 1E) (PTP-BAS, TYPE 1) (PROTEIN-
TYROSINE PHOSPHATASE PTPL1) (PROTEIN-TYROSINE PHOSPHATASE 1, FAS-ASSOCIATED)
(FAP-1).
GENBANK ACCESSION NO:Q92124 PHOSPHOTYROSYL-PROTEIN PHOSPHATASE (EC 3.1.3.48)
(PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:Q64503 PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, S
PRECURSOR (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:Q64504 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48)
(PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (FRAGMENT).
GENBANK ACCESSION NO:P2C3_SCHPO PROTEIN PHOSPHATASE 2C HOMOLOG 3 (EC 3.1.3.16)
(PP2C-3).
GENBANK ACCESSION NO:O48641 PROTEIN PHOSPHATASE 1 CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:Q15197 PROTEIN TYROSINE PHOSPHATASE (FRAGMENT).
GENBANK ACCESSION NO:Q27573 SERINE/THREONINE PROTEIN PHOSPHATASE (EC 3.1.3.16).
GENBANK ACCESSION NO:Q63294 LEUKOCYTE COMMON ANTIGEN RELATED PROTEIN (EC
3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q64509 PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 11
(EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE)
(PTPASE).
GENBANK ACCESSION NO:PP12_ACECL SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME
2 (EC 3.1.3.16).
GENBANK ACCESSION NO:P2B1_YEAST SERINE/THREONINE PROTEIN PHOSPHATASE 2B
CATALYTIC SUBUNIT A1 (EC 3.1.3.16) (CALCINEURIN A1) (CALMODULIN-BINDING PROTEIN
1).
GENBANK ACCESSION NO:Q63295 LEUCOCYTE COMMON ANTIGEN-RELATED PROTEIN (EC
3.1.3.48) (LAR) (FRAGMENT).
GENBANK ACCESSION NO:O35299 PROTEIN PHOSPHATASE 5.
GENBANK ACCESSION NO:Q63296 LEUCOCYTE COMMON ANTIGEN-RELATED PROTEIN (EC
3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:Q92682 PROTEIN-TYROSINE PHOSPHATASE NC-PTPCOM1 (EC
3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE).
GENBANK ACCESSION NO:Q9ZSS3 PROTEIN PHOSPHATASE 2A CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:PP1_ORYSA SERINE/THREONINE PROTEIN PHOSPHATASE PP1 (EC
3.1.3.16).
GENBANK ACCESSION NO:P2B_NEUCR SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC
SUBUNIT (EC 3.1.3.16) (CALMODULIN-DEPENDENT CALCINEURIN A SUBUNIT).
GENBANK ACCESSION NO:P2A1_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1
CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:YCCY_ECOLI PROBABLE LOW MOLECULAR WEIGHT PROTEIN-TYROSINE-
PHOSPHATASE YCCY (EC 3.1.3.48).
GENBANK ACCESSION NO:P78399 PROTEIN TYROSINE PHOSPHATASE RECEPTOR OMICRON (EC
3.1.3.48).
GENBANK ACCESSION NO:PTPJ_MOUSE PROTEIN-TYROSINE PHOSPHATASE ETA PRECURSOR (EC
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3.1.3.48) (R-PTP-ETA) (HPTP BETA-LIKE TYROSINE PHOSPHATASE).
GENBANK ACCESSION NO:PT17_STYPL PROTEIN-TYROSINE PHOSPHATASE 17 (EC 3.1.3.48) (FRAGMENT).
GENBANK ACCESSION NO:PP11_ARATH SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1 (EC 3.1.3.16).
GENBANK ACCESSION NO:Q9ZRF6 SERINE/THREONINE PROTEIN PHOSPHATASE 2A-3 CATALYTIC SUBUNIT.
GENBANK ACCESSION NO:Q64512 PROTEIN-TYROSINE PHOSPHATASE, NONRECEPTOR-TYPE, 13 (EC 3.1.3.48) (PROTEIN-TYROSINE PHOSPHATASE RIP) (PHOSPHOPROTEIN PHOSPHATASE) (PROTEIN-TYROSINE-PHOSPHATASE) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE) (PTP36).
GENBANK ACCESSION NO:O75702 PROTEIN-TYROSINE-PHOSPHATASE, ISOFORM 3 (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:O95063 LYMPHOID PHOSPHATASE LYP1 (EC 3.1.3.48).
GENBANK ACCESSION NO:O95064 LYMPHOID PHOSPHATASE LYP2 (EC 3.1.3.48).
GENBANK ACCESSION NO:O35385 PROTEIN PHOSPHATASE WITH EF-HANDS-2.
GENBANK ACCESSION NO:Q92850 RECEPTOR PROTEIN TYROSINE PHOSPHATASE PSI (EC 3.1.3.48).
GENBANK ACCESSION NO:O96914 PROTEIN SERINE/THREONINE PHOSPHATASE ALPHA.
GENBANK ACCESSION NO:P2AB_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-BETA, CATALYTIC SUBUNIT (EC 3.1.3.16).
GENBANK ACCESSION NO:P2A_PARTE SERINE/THREONINE PROTEIN PHOSPHATASE PP2A CATALYTIC SUBUNIT (EC 3.1.3.16) (PPN).
GENBANK ACCESSION NO:O88739 PROTEIN-TYROSINE-PHOSPHATASE (EC 3.1.3.48) (PHOSPHOTYROSINE PHOSPHATASE) (PTPASE).
GENBANK ACCESSION NO:Q91969 PROTEIN TYROSINE PHOSPHATASE PRECURSOR (EC 3.1.3.48).
GENBANK ACCESSION NO:PP12_TRYBB SERINE/THREONINE PROTEIN PHOSPHATASE PP1(5.9) (EC 3.1.3.16).
GENBANK ACCESSION NO:PP1B_HUMAN SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT (EC 3.1.3.16) (PP-1B).
GENBANK ACCESSION NO:O42205 PROTEIN PHOSPHATASE 5 (FRAGMENT).
GENBANK ACCESSION NO:PPP5_MOUSE SERINE/THREONINE PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).
GENBANK ACCESSION NO:PTN7_RAT PROTEIN-TYROSINE PHOSPHATASE LC-PTP (EC 3.1.3.48) (HEMATOPOIETIC PROTEIN-TYROSINE PHOSPHATASE) (HEPTP).
VH01 VACCC VH01 VACCC ID   VH01 VACCC   STANDARD;   PRT;   171 AA.
YOPH VACCC VH01 YOPH YERPS
PTN1 ID   PTN1 HUMAN   STANDARD;   PRT;   435 AA.
CDC25 GI|266561|SP|P30307|MPI3_HUMAN M-PHASE INDUCER PHOSPHATASE 3 (DUAL SPECIFICITY PHOSPHATASE CDC25C)
CDC14 YEAST GI|6321141|REF|NP_011219.1| SOLUBLE TYROSINE-SPECIFIC PROTEIN PHOSPHATASE; CDC14P [SACCHAROMYCES CEREVISIAE]
CDC14B_HUMAN GI|4502699|REF|NP_003662.1| S. CEREVISIAE CDC14 HOMOLOG, GENE B [HOMO SAPIENS]
CDC14A_HUMAN GI|4502697|REF|NP_003663.1| S. CEREVISIAE CDC14 HOMOLOG, GENE A [HOMO SAPIENS]

Table V.

Predicted exons of BMY_HPP4

Exon	Start	End	Sequence
1	71352	71414	CTCAGGCAGAACTATGAGGCCAAGAGTGCTCATGCGCACCAGGCTTTCTTTTTGAAAT TCGAG (SEQ ID NO:11)
2	71577	71667	GAGCTGAAGGAGGTGAGCAAGGAGCAGCCCAGACTGGAGGCTGAGTACCCTGCCAACA CCACCAAGAACTGTTAACCACATGTGCTACCCT (SEQ ID NO:12)
3	71776	71852	ATGACCACTCCAGGGTCAGGCTGACCCAGCTGGAGGGAGAGCCTCATTCTGACTACAT CAATGCCAACTTGGTCCCA (SEQ ID NO:13)
4	72885	73019	GGCTACACCCGCCCACAGGAGTTCATTGCCTCTCAGGGGCCTCTCAAGAAAACACTGG AGAACTTCTGGCGGCTGGTGCGGGAGCAGCAGGTCCGCATCATCATCATGCCGACCAT CAGCATGGAGAACGGGAGG (SEQ ID NO:14)
5	73700	73822	GTGCTGTGTGAGCATTACTGGCTGACCGACTCTACCCCGGACACCCATGGTCACATCA CCATCCACCTCCTAGCTGAGGAGCCTGAGGATGAGTGGACCAAGCGGGAATTCCAGCT GCAGCAC (SEQ ID NO:15)
6	74418	74578	GTTGTCCAGCAACATCAACGGAGGGTGGAGCAACTGCAGTTCACCACCTGATCCGACC ACAGCATCCTTGAGGCTCCCAGCTCCCTGCTCGCCTTTATGGAGCTGGTACAGTAGCA GGCAAGGGCCACCCAGGGCGTGGGACCCATCCTGGTGCACTGCAG (SEQ ID NO:16)
7	74700	74850	GGGCTGTCCCTGCGGTGTGGGCATGGGCCGGACAGGCACCTTCGTGGCCCTGTCGAGG CTGCTGCAGCAGCTGGAGGAGGAGCAGTTAGACGTGTTCCATGCTGTGTATGCAC TCCGGATGCACCAGCCCCTCATGATCCAGACCCTG (SEQ ID NO:17)
8	75210	75277	AGCCAGTACGTCTTCCTGCACAGCTGCCTACTGAACAAGATTCTGGAAGGACCCTTCA ACATCTCTGA (SEQ ID NO:18)
9	75407	75494	GTCTTGGCCCATCTCTGTGACGGACCTCCCGCAGGCGTGTGCCAAGAGGGCAGCCAGT GCCAATGCTGGCTTCTTGAAGGAGTACGAG (SEQ ID NO:19)
10	75613	75679	GCCATCAAGGACGAGGCTGGCTTTTCCGCACCCCCGCCTGGCTATGAGCAGGACAGCC CCGTCTCCT (SEQ ID NO:20)
11	75769	75826	ATGACCGTTCTCAGGGGCAGTTTTCTCCGGTGGAGGAGAGCCCCCCTGACGACATGCC (SEQ ID NO:21)
12	75960	76119	TCTCTGGAAGCCAATGATCTGTGCTCTGCAGGGTGGGCCCTCTGGCCGTGATCATACG GTGCTGACTGGCCCCGCAGGGCCAAAGGAGCTCTGGGAGCTGGTGTGGCAGCACAGGG TCATGTGCTTGTCTCTCTTTGCCCACCCAATGTCATGGAGAAG (SEQ ID NO:22)
13	76266	76376	GAATTCTGGCCAACGGAGATGCAGCCCGTAGTCACAGACATGGTGACGGTGCACTGGG TGGCTGAGAGCAGCACAGCAGGCTGGTTCTGTACCCTCCTCAGGGTCACACAT (SEQ ID NO:23)
14	76481	76644	GGGGAGAGCAGGAAGGAAAGGGAGGTGCAGAGACTGCAATTTCCATACCTGGAGCCTG GGCATGAGCTGCCCGCCACCACCCTGCTGCCCTTCCTGGCTGCTGTGGGCCAGTGCTG CTCTCGGGGCAACAACAAGAAGCCGGGCACACTGCTCAGCCACTCCAA (SEQ ID NO:24)
15	76992	77127	CAAGGGTGCAACCCAGCTGGGCACCTTCCTGGCCATGGAGCAGCTGCTGCAGCAGGCA GGGTCTGAGTGCACCGTGGATATCTTTAACGTGGCCCTGCAGCAGTCTCAGGCCTGTG GCCTTATGACCCCAACACTG (SEQ ID NO:25)
16	77369	77425	AAGCAGTATGTCTACCTCTACAACTGTCTGAACAGCGCGCTGGCAGACAGGGCTGCCC (SEQ ID NO:26)

Table VI

Gene	Left Cloning Primer	Right Cloning Primer	Internal RevComp Cloning Primer	Internal Cloning Primer	EP Sense Primer	EP Anti-Sense Primer
BMY_HPP1	CGGATGGAAGGATTATGGTG (SEQ ID NO.45)	CTGTTCGACCAAGCC CTG (SEQ ID NO.44)	TGACAATGGATAGCTACTTTCCTTCTCCT GTAAGGCAAATGTCATCCACCTCACCAT ATCTAGGATAGTAGTAAGAAGACGC (SEQ ID NO.45)	N/A	TACAATTCGGATGGAA GGATTAT (SEQ ID NO.154)	GCATGACAATGGATAGCTA CTTT (SEQ ID NO.155)
"	TTCGGATGGAAGGATTATGG (SEQ ID NO.46)	CTGTTCGACCAAGCC CTG (SEQ ID NO.47)	TGACAATGGATAGCTACTTTTCCTTCTCCT GTAAGGCAAATGTCATCCACCTTCACCAT ATCTAGGATAGTAGTAAGAAGACGC (SEQ ID NO.48)	N/A	N/A	N/A
BMY_HPP2	CCAACTTCTCCTGGGTGCT (SEQ ID NO.49)	CTCCGTCAGGGACAC CAG (SEQ ID NO.50)	GTCGCGCAGGCCAGGTCCAACAGGAA CTGGTAGTGCGGGGGAGCGCGGCAG CGCCAGTCCCGCCAGCCGGCCGGA (SEQ ID NO.51)	N/A	GAGAAGCAGTCTTCCAGT TCTAC (SEQ ID NO.156)	ATGGGAGCTAGAGCGGTTTAAT ACT (SEQ ID NO.157)
"	CAACTTCTCCTGGGTGCCTTC (SEQ ID NO.52)	CAGCTGTGTCGTCTGA GGG (SEQ ID NO.53)	CTCCGTCAGGGACACCAGGTGCCGCAC GCCCAGTCCAACAGGAACTGGTAGTG GGCCGGGAGCGCGCAGCCGGCCAGTC (SEQ ID NO.54)	N/A	N/A	N/A
BMY_HPP3	CTCCTTGCTCTGTGGGACAT (SEQ ID NO.55)	AACCTGGATGCTTCC CTTCT (SEQ ID NO.56)	AAAAGAGGCAAATGTTGTAAGTTGCTTTTC ATACTTCTACTATGGTGGTAACTCCATC CTGCTTAAGTTCCTGTAAGAAATCT (SEQ ID NO.57)	N/A	N/A	N/A
"	TGCTCTGTGGACATTGCAT (SEQ ID NO.58)	AACCTGGATGCTTCC CTTCT (SEQ ID NO.59)	AAAAGAGGCAATGTTGTAAGTTGCTTTTC ATACTTCTACTATGGTGGTAACTCCATC CTGCTTAAGTTCCTGTAAGAAATCT (SEQ ID NO.60)	N/A	N/A	N/A
BMY_HPP4	GGCAGGAACTATGAGGCCAA G (SEQ ID NO.61)	GACCCTGGAGTGGTC ATAGG (SEQ ID NO.62)	GGTCATGGGCACCAGGCTTTTTTTGA AATTCGAAGGCGCTGAAGGAAGGTGAGCA AGGAGCAGCCCAGACTGGAGGCTGA (SEQ ID NO.63)	N/A	N/A	N/A
"	GCACCCAGGCTTTTCTTTTGA (SEQ ID NO.64)	GACCCTGGAGTGGTC ATAGG (SEQ ID NO.65)	TCGAGGCAGGCTGAAGGAGGTGAGGGAAGG AGCAGCCCAGACTGGAGGCTGAGTACC CTGCCAACACCACCAAGAACTGTTAA (SEQ ID NO.66)	N/A	N/A	N/A
"	AGGCAGAACTATGAGGCCA A (SEQ ID NO.71)	GACCCTGGAGTGGTC ATAGG (SEQ ID NO.72)	TCAGCTCCAGTCTGGGCTGCTCCTTGC TCACCTCCTTCAGCTCCTCGAATTTCAA AAAGAAAAGCCTGGTGCCGCATGAGC (SEQ ID NO.74)	GCTCATGCGCACCAGG CTTTCTTTTTGAAAATTC GAGGAGCTGAAGGAG GTGAGCAAGGAGCAGC CCAGACTGGAGGCTGA (SEQ ID NO. 75)	N/A	N/A
BMY_HPP5	GGCCAAAGGACGAAACTCAA G (SEQ ID NO.69)	GCATAGCTTGTTGGT CCCAT (SEQ ID NO.70)	N/A	N/A	ATGGGAGCCAACAAGCCA TGC (SEQ ID NO.67)	TTATCAGGACTGGTTTCGG G (SEQ ID NO.68)

TableVIII

Atom No	Atom name	Residue	Residue No	X coord	Y coord	Z coord
1	N	MET	1	69.582	18.182	8.672
2	CA	MET	1	69.395	19.541	8.131
3	C	MET	1	70.570	19.947	7.256
4	O	MET	1	70.396	20.201	6.059
5	CB	MET	1	69.269	20.550	9.267
6	CG	MET	1	68.073	20.254	10.160
7	SD	MET	1	67.870	21.392	11.549
8	CE	MET	1	67.694	22.936	10.625
9	N	ALA	2	71.766	19.777	7.798
10	CA	ALA	2	72.997	20.244	7.135
11	C	ALA	2	73.470	19.379	5.963
12	O	ALA	2	74.399	19.766	5.248
13	CB	ALA	2	74.103	20.321	8.182
14	N	ALA	3	72.827	18.242	5.755
15	CA	ALA	3	73.118	17.415	4.583
16	C	ALA	3	72.087	17.628	3.469
17	O	ALA	3	72.257	17.097	2.366
18	CB	ALA	3	73.129	15.952	5.009
19	N	GLY	4	71.058	18.418	3.754
20	CA	GLY	4	69.967	18.671	2.798
21	C	GLY	4	69.309	17.377	2.327
22	O	GLY	4	69.228	17.114	1.124
23	N	VAL	5	68.792	16.606	3.271
24	CA	VAL	5	68.290	15.269	2.935
25	C	VAL	5	67.085	14.887	3.803
26	O	VAL	5	66.835	13.713	4.111
27	CB	VAL	5	69.467	14.309	3.108
28	CG1	VAL	5	69.856	14.148	4.572
29	CG2	VAL	5	69.222	12.952	2.454
30	N	LEU	6	66.245	15.878	4.045
31	CA	LEU	6	65.060	15.698	4.912
32	C	LEU	6	64.105	14.540	4.542
33	O	LEU	6	63.856	13.736	5.454
34	CB	LEU	6	64.282	17.010	5.011
35	CG	LEU	6	64.512	17.720	6.344
36	CD1	LEU	6	64.147	16.806	7.510
37	CD2	LEU	6	65.943	18.232	6.500
38	N	PRO	7	63.677	14.339	3.292
39	CA	PRO	7	62.757	13.220	3.028
40	C	PRO	7	63.352	11.816	3.190
41	O	PRO	7	62.579	10.904	3.506
42	CB	PRO	7	62.275	13.409	1.625
43	CG	PRO	7	63.027	14.558	0.983
44	CD	PRO	7	63.918	15.128	2.068
45	N	GLN	8	64.670	11.673	3.259
46	CA	GLN	8	65.250	10.338	3.447
47	C	GLN	8	65.289	9.903	4.908
48	O	GLN	8	65.636	8.751	5.182
49	CB	GLN	8	66.654	10.268	2.873
50	CG	GLN	8	66.628	10.270	1.352
51	CD	GLN	8	68.031	9.988	0.833
52	OE1	GLN	8	68.459	10.546	−0.184
53	NE2	GLN	8	68.740	9.136	1.554
54	N	ASN	9	64.901	10.785	5.815
55	CA	ASN	9	64.698	10.384	7.205
56	C	ASN	9	63.244	9.968	7.410
57	O	ASN	9	62.944	9.083	8.221
58	CB	ASN	9	64.990	11.583	8.104
59	CG	ASN	9	66.375	12.157	7.822
60	OD1	ASN	9	67.397	11.480	7.985
61	ND2	ASN	9	66.392	13.417	7.424

62	N	GLU	10	62.390	10.452	6.522
63	CA	GLU	10	60.956	10.177	6.614
64	C	GLU	10	60.605	8.894	5.876
65	O	GLU	10	59.725	8.146	6.320
66	CB	GLU	10	60.222	11.364	6.002
67	CG	GLU	10	60.573	12.649	6.745
68	CD	GLU	10	60.015	13.867	6.017
69	OE1	GLU	10	60.266	13.966	4.824
70	OE2	GLU	10	59.569	14.781	6.701
71	N	GLN	11	61.423	8.553	4.896
72	CA	GLN	11	61.272	7.276	4.185
73	C	GLN	11	61.393	6.035	5.090
74	O	GLN	11	60.421	5.272	5.090
75	CB	GLN	11	62.255	7.214	3.018
76	CG	GLN	11	61.929	8.252	1.948
77	CD	GLN	11	60.572	7.967	1.301
78	OE1	GLN	11	60.424	7.000	0.547
79	NE2	GLN	11	59.615	8.842	1.563
80	N	PRO	12	62.416	5.858	5.928
81	CA	PRO	12	62.396	4.703	6.838
82	C	PRO	12	61.285	4.734	7.899
83	O	PRO	12	60.776	3.655	8.219
84	CB	PRO	12	63.740	4.679	7.498
85	CG	PRO	12	64.528	5.909	7.086
86	CD	PRO	12	63.643	6.651	6.104
87	N	TYR	13	60.721	5.892	8.217
88	CA	TYR	13	59.612	5.912	9.181
89	C	TYR	13	58.322	5.470	8.496
90	O	TYR	13	57.589	4.648	9.058
91	CB	TYR	13	59.435	7.317	9.750
92	CG	TYR	13	60.630	7.853	10.531
93	CD1	TYR	13	60.876	9.220	10.549
94	CD2	TYR	13	61.455	6.986	11.238
95	CE1	TYR	13	61.970	9.718	11.243
96	CE2	TYR	13	62.551	7.482	11.931
97	CZ	TYR	13	62.810	8.846	11.923
98	OH	TYR	13	63.964	9.325	12.505
99	N	SER	14	58.271	5.707	7.194
100	CA	SER	14	57.170	5.235	6.347
101	C	SER	14	57.337	3.768	5.941
102	O	SER	14	56.452	3.205	5.291
103	CB	SER	14	57.142	6.091	5.085
104	OG	SER	14	57.018	7.452	5.473
105	N	THR	15	58.452	3.163	6.315
106	CA	THR	15	58.670	1.739	6.078
107	C	THR	15	58.496	0.951	7.378
108	O	THR	15	58.252	−0.261	7.356
109	CB	THR	15	60.094	1.583	5.555
110	OG1	THR	15	60.252	2.470	4.457
111	CG2	THR	15	60.388	0.165	5.079
112	N	LEU	16	58.570	1.658	8.496
113	CA	LEU	16	58.401	1.037	9.818
114	C	LEU	16	56.980	1.194	10.354
115	O	LEU	16	56.624	0.571	11.363
116	CB	LEU	16	59.374	1.694	10.792
117	CG	LEU	16	60.826	1.428	10.409
118	CD1	LEU	16	61.781	2.252	11.266
119	CD2	LEU	16	61.158	−0.058	10.496
120	N	VAL	17	56.197	2.008	9.664
121	CA	VAL	17	54.788	2.266	9.995
122	C	VAL	17	53.993	2.271	10.214
123	O	VAL	17	54.216	−0.044	9.539
124	CB	VAL	17	54.229	3.071	8.820
125	CG1	VAL	17	54.351	2.306	7.509
126	CG2	VAL	17	52.795	3.523	9.037

127	N	ASN	18	53.139	0.982	11.226
128	CA	ASN	18	52.379	−0.223	11.563
129	C	ASN	18	51.049	−0.245	10.820
130	O	ASN	18	50.052	0.386	11.194
131	CB	ASN	18	52.174	−0.298	13.069
132	CG	ASN	18	53.534	−0.362	13.762
133	OD1	ASN	18	53.935	0.571	14.468
134	ND2	ASN	18	54.237	−1.459	13.540
135	N	ASN	19	51.075	−1.017	9.750
136	CA	ASN	19	49.936	−1.159	8.843
137	C	ASN	19	48.936	−2.200	9.350
138	O	ASN	19	49.078	−3.402	9.100
139	CB	ASN	19	50.500	−1.593	7.491
140	CG	ASN	19	51.685	−0.700	7.116
141	OD1	ASN	19	51.561	0.529	7.063
142	ND2	ASN	19	52.818	−1.333	6.852
143	N	SER	20	47.949	−1.721	10.088
144	CA	SER	20	46.889	−2.590	10.618
145	C	SER	20	45.830	−2.891	9.562
146	O	SER	20	45.525	−2.040	8.721
147	CB	SER	20	46.232	−1.875	11.801
148	OG	SER	20	45.102	−2.630	12.237
149	N	GLU	21	45.339	−4.120	9.571
150	CA	GLU	21	44.151	−4.470	8.780
151	C	GLU	21	42.990	−3.623	9.296
152	O	GLU	21	42.894	−3.409	10.508
153	CB	GLU	21	43.865	−5.955	8.991
154	CG	GLU	21	42.687	−6.464	8.166
155	CD	GLU	21	42.494	−7.954	8.426
156	OE1	GLU	21	43.469	−8.582	8.815
157	OE2	GLU	21	41.380	−8.429	8.263
158	N	CYS	22	42.217	−3.047	8.392
159	CA	CYS	22	41.161	−2.120	8.792
160	C	CYS	22	39.765	−2.693	8.569
161	O	CYS	22	39.563	−3.630	7.786
162	CB	CYS	22	41.360	−0.857	7.974
163	SG	CYS	22	43.044	−0.206	8.046
164	N	VAL	23	38.801	−2.093	9.248
165	CA	VAL	23	37.410	−2.559	9.153
166	C	VAL	23	36.644	−1.812	8.059
167	O	VAL	23	35.572	−2.256	7.621
168	CB	VAL	23	36.740	−2.372	10.516
169	CG1	VAL	23	36.590	−0.899	10.877
170	CG2	VAL	23	35.391	−3.076	10.594
171	N	ALA	24	37.294	−0.816	7.480
172	CA	ALA	24	36.669	0.010	6.445
173	C	ALA	24	36.847	−0.557	5.038
174	O	ALA	24	36.343	0.014	4.069
175	CB	ALA	24	37.252	1.412	6.533
176	N	ASN	25	37.456	−1.729	4.950
177	CA	ASN	25	37.721	−2.366	3.660
178	C	ASN	25	36.534	−3.178	3.137
179	O	ASN	25	36.524	−3.565	1.963
180	CB	ASN	25	38.930	−3.280	3.838
181	CG	ASN	25	40.179	−2.458	4.151
182	OD1	ASN	25	40.470	−2.127	5.308
183	ND2	ASN	25	40.901	−2.124	3.099
184	N	MET	26	35.538	−3.416	3.977
185	CA	MET	26	34.328	−4.102	3.504
186	C	MET	26	33.381	−3.091	2.866
187	O	MET	26	33.376	−1.924	3.270
188	CB	MET	26	33.654	−4.832	4.661
189	CG	MET	26	33.177	−3.886	5.754
190	SD	MET	26	32.426	−4.700	7.181
191	CE	MET	26	33.870	−5.620	7.759

192	N	LYS	27	32.484	-3.577	2.021
193	CA	LYS	27	31.626	-2.711	1.187
194	C	LYS	27	30.792	-1.697	1.974
195	O	LYS	27	30.871	-0.498	1.677
196	CB	LYS	27	30.697	-3.613	0.383
197	CG	LYS	27	29.798	-2.809	-0.555
198	CD	LYS	27	28.844	-3.672	-1.388
199	CE	LYS	27	29.482	-4.306	-2.629
200	NZ	LYS	27	30.336	-5.470	-2.332
201	N	GLY	28	30.225	-2.129	3.092
202	CA	GLY	28	29.458	-1.231	3.969
203	C	GLY	28	30.290	-0.040	4.450
204	O	GLY	28	29.996	1.104	4.083
205	N	ASN	29	31.466	-0.337	4.977
206	CA	ASN	29	32.335	0.704	5.533
207	C	ASN	29	33.239	1.388	4.500
208	O	ASN	29	33.918	2.358	4.860
209	CB	ASN	29	33.195	0.102	6.632
210	CG	ASN	29	32.343	-0.411	7.789
211	OD1	ASN	29	31.243	0.082	8.065
212	ND2	ASN	29	32.880	-1.409	8.463
213	N	LEU	30	33.112	1.040	3.226
214	CA	LEU	30	33.875	1.715	2.163
215	C	LEU	30	33.311	3.095	1.834
216	O	LEU	30	34.001	3.921	1.228
217	CB	LEU	30	33.839	0.868	0.893
218	CG	LEU	30	34.861	-0.261	0.909
219	CD1	LEU	30	34.663	-1.187	-0.285
220	CD2	LEU	30	36.278	0.297	0.916
221	N	GLU	31	32.115	3.379	2.326
222	CA	GLU	31	31.537	4.722	2.198
223	C	GLU	31	31.873	5.616	3.401
224	O	GLU	31	31.357	6.738	3.502
225	CB	GLU	31	30.029	4.560	2.047
226	CG	GLU	31	29.433	3.878	3.269
227	CD	GLU	31	28.144	3.156	2.901
228	OE1	GLU	31	28.003	2.802	1.740
229	OE2	GLU	31	27.327	2.949	3.791
230	N	ARG	32	32.699	5.117	4.310
231	CA	ARG	32	33.060	5.883	5.506
232	C	ARG	32	34.325	6.737	5.316
233	O	ARG	32	34.177	7.964	5.387
234	CB	ARG	32	33.155	4.948	6.710
235	CG	ARG	32	31.839	4.213	6.909
236	CD	ARG	32	31.781	3.498	8.249
237	NE	ARG	32	30.378	3.247	8.608
238	CZ	ARG	32	29.731	3.986	9.510
239	NH1	ARG	32	30.398	4.885	10.237
240	NH2	ARG	32	28.440	3.757	9.756
241	N	PRO	33	35.516	6.182	5.096
242	CA	PRO	33	36.646	7.045	4.744
243	C	PRO	33	36.534	7.511	3.299
244	O	PRO	33	36.825	6.765	2.356
245	CB	PRO	33	37.868	6.204	4.929
246	CG	PRO	33	37.438	4.755	5.064
247	CD	PRO	33	35.920	4.768	5.055
248	N	THR	34	36.102	8.749	3.141
249	CA	THR	34	35.990	9.338	1.799
250	C	THR	34	37.323	9.447	1.024
251	O	THR	34	37.283	9.160	-0.179
252	CB	THR	34	35.246	10.673	1.873
253	OG1	THR	34	35.822	11.478	2.892
254	CG2	THR	34	33.783	10.455	2.243
255	N	PRO	35	38.464	9.823	1.599
256	CA	PRO	35	39.706	9.336	0.998

257	C	PRO	35	39.844	7.831	1.226
258	O	PRO	35	40.187	7.406	2.336
259	CB	PRO	35	40.802	10.087	1.689
260	CG	PRO	35	40.226	10.777	2.914
261	CD	PRO	35	38.737	10.475	2.893
262	N	LYS	36	39.863	7.088	0.128
263	CA	LYS	36	39.914	5.614	0.169
264	C	LYS	36	41.286	5.061	0.579
265	O	LYS	36	41.397	3.917	1.032
266	CB	LYS	36	39.577	5.120	-1.237
267	CG	LYS	36	39.491	3.599	-1.326
268	CD	LYS	36	39.361	3.134	-2.772
269	CE	LYS	36	38.129	3.728	-3.447
270	NZ	LYS	36	38.033	3.283	-4.847
271	N	TYR	37	42.295	5.915	0.564
272	CA	TYR	37	43.631	5.512	1.004
273	C	TYR	37	43.846	5.752	2.502
274	O	TYR	37	44.880	5.347	3.045
275	CB	TYR	37	44.681	6.269	0.185
276	CG	TYR	37	44.657	7.798	0.284
277	CD1	TYR	37	45.380	8.439	1.284
278	CD2	TYR	37	43.942	8.550	-0.642
279	CE1	TYR	37	45.363	9.824	1.378
280	CE2	TYR	37	43.923	9.935	-0.550
281	CZ	TYR	37	44.630	10.568	0.464
282	OH	TYR	37	44.587	11.941	0.577
283	N	THR	38	42.871	6.340	3.176
284	CA	THR	38	43.050	6.648	4.596
285	C	THR	38	42.213	5.707	5.456
286	O	THR	38	41.131	6.059	5.941
287	CB	THR	38	42.641	8.094	4.837
288	OG1	THR	38	43.174	8.881	3.782
289	CG2	THR	38	43.202	8.609	6.156
290	N	LYS	39	42.750	4.519	5.663
291	CA	LYS	39	42.036	3.494	6.428
292	C	LYS	39	42.502	3.416	7.886
293	O	LYS	39	43.693	3.264	8.184
294	CB	LYS	39	42.239	2.161	5.716
295	CG	LYS	39	41.590	2.151	4.335
296	CD	LYS	39	40.076	2.292	4.440
297	CE	LYS	39	39.405	2.337	3.072
298	NZ	LYS	39	39.662	1.106	2.313
299	N	VAL	40	41.531	3.529	8.777
300	CA	VAL	40	41.769	3.425	10.225
301	C	VAL	40	41.831	1.958	10.671
302	O	VAL	40	40.993	1.144	10.260
303	CB	VAL	40	40.638	4.187	10.919
304	CG1	VAL	40	39.268	3.784	10.385
305	CG2	VAL	40	40.691	4.087	12.438
306	N	GLY	41	42.816	1.646	11.505
307	CA	GLY	41	43.080	0.269	11.961
308	C	GLY	41	41.885	-0.455	12.586
309	O	GLY	41	40.856	0.143	12.912
310	N	GLU	42	42.086	-1.735	12.843
311	CA	GLU	42	40.995	-2.603	13.318
312	C	GLU	42	40.700	-2.470	14.817
313	O	GLU	42	39.903	-1.616	15.224
314	CB	GLU	42	41.372	-4.056	13.016
315	CG	GLU	42	40.208	-5.037	13.176
316	CD	GLU	42	39.111	-4.717	12.172
317	OE1	GLU	42	39.427	-4.667	10.996
318	OE2	GLU	42	38.001	-4.442	12.611
319	N	ARG	43	41.515	-3.159	15.603
320	CA	ARG	43	41.196	-3.553	16.987
321	C	ARG	43	41.019	-2.475	18.056

322	O	ARG	43	40.698	-1.315	17.771
323	CB	ARG	43	42.252	-4.560	17.413
324	CG	ARG	43	42.024	-5.844	16.627
325	CD	ARG	43	43.145	-6.861	16.793
326	NE	ARG	43	42.810	-8.099	16.069
327	CZ	ARG	43	43.092	-8.326	14.782
328	NH1	ARG	43	42.660	-9.446	14.197
329	NH2	ARG	43	43.743	-7.410	14.061
330	N	LEU	44	41.420	-2.857	19.260
331	CA	LEU	44	40.940	-2.274	20.535
332	C	LEU	44	41.307	-0.825	20.889
333	O	LEU	44	40.872	-0.346	21.941
334	CB	LEU	44	41.471	-3.171	21.649
335	CG	LEU	44	40.988	-4.610	21.499
336	CD1	LEU	44	41.711	-5.534	22.473
337	CD2	LEU	44	39.476	-4.712	21.677
338	N	ARG	45	42.074	-0.139	20.064
339	CA	ARG	45	42.359	1.270	20.330
340	C	ARG	45	42.277	2.045	19.017
341	O	ARG	45	42.438	3.271	18.953
342	CB	ARG	45	43.741	1.367	20.972
343	CG	ARG	45	44.040	2.774	21.469
344	CD	ARG	45	45.316	2.817	22.295
345	NE	ARG	45	45.143	2.075	23.552
346	CZ	ARG	45	46.140	1.431	24.157
347	NH1	ARG	45	47.350	1.403	23.596
348	NH2	ARG	45	45.919	0.787	25.305
349	N	HIS	46	41.904	1.325	17.978
350	CA	HIS	46	41.969	1.898	16.641
351	C	HIS	46	40.653	2.581	16.302
352	O	HIS	46	40.472	3.723	16.742
353	CB	HIS	46	42.340	0.803	15.655
354	CG	HIS	46	43.700	0.165	15.909
355	ND1	HIS	46	44.770	0.745	16.483
356	CD2	HIS	46	44.075	-1.114	15.581
357	CE1	HIS	46	45.787	-0.136	16.538
358	NE2	HIS	46	45.357	-1.287	15.976
359	N	VAL	47	39.754	1.908	15.599
360	CA	VAL	47	38.471	2.532	15.221
361	C	VAL	47	37.658	2.971	16.434
362	O	VAL	47	37.399	2.178	17.348
363	CB	VAL	47	37.650	1.541	14.392
364	CG1	VAL	47	36.163	1.879	14.354
365	CG2	VAL	47	38.190	1.434	12.977
366	N	ILE	48	37.362	4.260	16.470
367	CA	ILE	48	36.458	4.827	17.472
368	C	ILE	48	35.032	4.352	17.216
369	O	ILE	48	34.421	4.650	16.181
370	CB	ILE	48	36.563	6.348	17.385
371	CG1	ILE	48	37.887	6.817	17.971
372	CG2	ILE	48	35.404	7.035	18.090
373	CD1	ILE	48	37.969	6.480	19.456
374	N	PRO	49	34.540	3.554	18.149
375	CA	PRO	49	33.270	2.865	17.959
376	C	PRO	49	32.085	3.791	18.185
377	O	PRO	49	32.083	4.621	19.102
378	CB	PRO	49	33.270	1.770	18.979
379	CG	PRO	49	34.423	1.991	19.946
380	CD	PRO	49	35.204	3.174	19.399
381	N	GLY	50	31.104	3.670	17.312
382	CA	GLY	50	29.816	4.304	17.576
383	C	GLY	50	29.050	3.408	18.537
384	O	GLY	50	29.066	2.179	18.400
385	N	HIS	51	28.351	4.019	19.478
386	CA	HIS	51	27.698	3.254	20.556

387	C	HIS	51	26.280	2.772	20.229
388	O	HIS	51	25.346	3.003	21.005
389	CB	HIS	51	27.673	4.099	21.828
390	CG	HIS	51	28.989	4.180	22.588
391	ND1	HIS	51	29.133	4.531	23.880
392	CD2	HIS	51	30.253	3.914	22.109
393	CE1	HIS	51	30.439	4.492	24.214
394	NE2	HIS	51	31.130	4.112	23.117
395	N	MET	52	26.136	2.082	19.109
396	CA	MET	52	24.848	1.485	18.743
397	C	MET	52	25.075	0.169	18.005
398	O	MET	52	25.986	0.049	17.177
399	CB	MET	52	24.018	2.457	17.907
400	CG	MET	52	24.634	2.773	16.550
401	SD	MET	52	23.695	3.953	15.554
402	CE	MET	52	22.077	3.150	15.606
403	N	ALA	53	24.147	-0.754	18.204
404	CA	ALA	53	24.284	-2.128	17.691
405	C	ALA	53	23.978	-2.325	16.202
406	O	ALA	53	24.059	-3.457	15.713
407	CB	ALA	53	23.376	-3.036	18.512
408	N	CYS	54	23.645	-1.260	15.491
409	CA	CYS	54	23.405	-1.382	14.053
410	C	CYS	54	24.734	-1.431	13.308
411	O	CYS	54	25.184	-2.517	12.923
412	CB	CYS	54	22.566	-0.201	13.582
413	SG	CYS	54	20.908	-0.110	14.297
414	N	SER	55	25.369	-0.277	13.169
415	CA	SER	55	26.666	-0.190	12.481
416	C	SER	55	27.231	1.228	12.501
417	O	SER	55	26.638	2.156	11.940
418	CB	SER	55	26.511	-0.655	11.034
419	OG	SER	55	25.477	0.106	10.424
420	N	MET	56	28.353	1.384	13.187
421	CA	MET	56	29.096	2.656	13.196
422	C	MET	56	30.600	2.436	13.331
423	O	MET	56	31.173	2.695	14.400
424	CB	MET	56	28.646	3.551	14.348
425	CG	MET	56	27.381	4.345	14.049
426	SD	MET	56	26.900	5.538	15.320
427	CE	MET	56	28.370	6.588	15.307
428	N	ALA	57	31.242	2.052	12.240
429	CA	ALA	57	32.706	1.893	12.247
430	C	ALA	57	33.392	3.145	11.700
431	O	ALA	57	33.988	3.123	10.616
432	CB	ALA	57	33.076	0.686	11.397
433	N	CYS	58	33.390	4.185	12.518
434	CA	CYS	58	33.824	5.524	12.102
435	C	CYS	58	35.305	5.618	11.734
436	O	CYS	58	36.155	4.864	12.227
437	CB	CYS	58	33.512	6.469	13.251
438	SG	CYS	58	31.786	6.444	13.783
439	N	GLY	59	35.596	6.575	10.865
440	CA	GLY	59	36.968	6.800	10.382
441	C	GLY	59	37.774	7.717	11.303
442	O	GLY	59	38.007	8.895	10.997
443	N	GLY	60	38.232	7.142	12.401
444	CA	GLY	60	39.017	7.884	13.390
445	C	GLY	60	39.619	6.940	14.424
446	O	GLY	60	38.932	6.039	14.914
447	N	ARG	61	40.895	7.121	14.717
448	CA	ARG	61	41.560	6.257	15.705
449	C	ARG	61	41.929	6.985	16.991
450	O	ARG	61	42.244	8.181	16.984
451	CB	ARG	61	42.771	5.545	15.095

452	CG	ARG	61	43.632	6.425	14.197
453	CD	ARG	61	44.466	7.462	14.939
454	NE	ARG	61	45.563	6.879	15.722
455	CZ	ARG	61	46.833	7.006	15.334
456	NH1	ARG	61	47.823	6.728	16.183
457	NH2	ARG	61	47.107	7.616	14.183
458	N	ALA	62	41.903	6.251	18.089
459	CA	ALA	62	42.264	6.837	19.383
460	C	ALA	62	43.750	6.672	19.674
461	O	ALA	62	44.193	5.620	20.148
462	CB	ALA	62	41.458	6.156	20.482
463	N	CYS	63	44.500	7.745	19.497
464	CA	CYS	63	45.938	7.694	19.774
465	C	CYS	63	46.234	7.938	21.252
466	O	CYS	63	46.357	9.083	21.706
467	CB	CYS	63	46.645	8.743	18.931
468	SG	CYS	63	48.445	8.739	19.045
469	N	LYS	64	46.226	6.848	22.001
470	CA	LYS	64	46.613	6.860	23.412
471	C	LYS	64	48.054	6.384	23.552
472	O	LYS	64	48.406	5.291	23.091
473	CB	LYS	64	45.675	5.924	24.169
474	CG	LYS	64	46.126	5.674	25.604
475	CD	LYS	64	45.182	4.716	26.320
476	CE	LYS	64	45.706	4.351	27.703
477	NZ	LYS	64	47.001	3.660	27.607
478	N	TYR	65	48.885	7.218	24.151
479	CA	TYR	65	50.292	6.848	24.356
480	C	TYR	65	50.417	5.930	25.573
481	O	TYR	65	50.529	6.362	26.725
482	CB	TYR	65	51.115	8.124	24.463
483	CG	TYR	65	51.006	8.959	23.186
484	CD1	TYR	65	50.248	10.122	23.169
485	CD2	TYR	65	51.651	8.538	22.030
486	CE1	TYR	65	50.138	10.869	22.004
487	CE2	TYR	65	51.545	9.283	20.862
488	CZ	TYR	65	50.789	10.448	20.853
489	OH	TYR	65	50.703	11.202	19.702
490	N	GLU	66	50.503	4.650	25.250
491	CA	GLU	66	50.281	3.565	26.211
492	C	GLU	66	51.266	3.423	27.361
493	O	GLU	66	52.477	3.638	27.234
494	CB	GLU	66	50.240	2.244	25.435
495	CG	GLU	66	51.547	1.850	24.735
496	CD	GLU	66	52.510	1.069	25.640
497	OE1	GLU	66	52.038	0.495	26.612
498	OE2	GLU	66	53.675	0.978	25.281
499	N	ASN	67	50.676	3.106	28.499
500	CA	ASN	67	51.379	2.400	29.576
501	C	ASN	67	50.476	1.416	30.372
502	O	ASN	67	50.631	1.373	31.597
503	CB	ASN	67	51.998	3.439	30.515
504	CG	ASN	67	50.965	4.467	30.982
505	OD1	ASN	67	49.852	4.121	31.398
506	ND2	ASN	67	51.342	5.730	30.899
507	N	PRO	68	49.614	0.599	29.756
508	CA	PRO	68	48.551	−0.034	30.556
509	C	PRO	68	48.957	−1.352	31.228
510	O	PRO	68	48.432	−1.685	32.297
511	CB	PRO	68	47.449	−0.296	29.577
512	CG	PRO	68	48.006	−0.199	28.167
513	CD	PRO	68	49.432	0.295	28.323
514	N	ALA	69	49.875	−2.081	30.617
515	CA	ALA	69	50.325	−3.359	31.167
516	C	ALA	69	51.279	−3.132	32.327

517	O	ALA	69	51.904	-2.070	32.438
518	CB	ALA	69	51.024	-4.157	30.072
519	N	ARG	70	51.339	-4.116	33.206
520	CA	ARG	70	52.260	-4.056	34.338
521	C	ARG	70	53.692	-3.993	33.818
522	O	ARG	70	54.103	-4.803	32.978
523	CB	ARG	70	52.044	-5.292	35.204
524	CG	ARG	70	52.811	-5.206	36.519
525	CD	ARG	70	52.437	-6.363	37.438
526	NE	ARG	70	50.978	-6.406	37.637
527	CZ	ARG	70	50.356	-5.922	38.715
528	NH1	ARG	70	51.061	-5.383	39.713
529	NH2	ARG	70	49.026	-5.996	38.804
530	N	TRP	71	54.353	-2.913	34.207
531	CA	TRP	71	55.728	-2.595	33.803
532	C	TRP	71	55.796	-2.191	32.323
533	O	TRP	71	56.612	-2.714	31.553
534	CB	TRP	71	56.646	-3.779	34.113
535	CG	TRP	71	58.131	-3.471	34.056
536	CD1	TRP	71	58.826	-2.625	34.894
537	CD2	TRP	71	59.090	-3.999	33.115
538	NE1	TRP	71	60.126	-2.615	34.511
539	CE2	TRP	71	60.328	-3.422	33.451
540	CE3	TRP	71	58.998	-4.885	32.055
541	CZ2	TRP	71	61.460	-3.735	32.710
542	CZ3	TRP	71	60.132	-5.193	31.316
543	CH2	TRP	71	61.358	-4.623	31.643
544	N	SER	72	54.883	-1.327	31.909
545	CA	SER	72	55.032	-0.686	30.599
546	C	SER	72	55.985	0.489	30.750
547	O	SER	72	55.906	1.236	31.731
548	CB	SER	72	53.687	-0.207	30.082
549	OG	SER	72	52.882	-1.347	29.831
550	N	GLU	73	56.853	0.672	29.773
551	CA	GLU	73	57.920	1.661	29.944
552	C	GLU	73	57.522	3.093	29.602
553	O	GLU	73	57.643	3.941	30.493
554	CB	GLU	73	59.110	1.268	29.076
555	CG	GLU	73	60.262	2.254	29.257
556	CD	GLU	73	61.423	1.890	28.339
557	OE1	GLU	73	62.144	0.964	28.684
558	OE2	GLU	73	61.479	2.443	27.251
559	N	GLN	74	56.848	3.279	28.472
560	CA	GLN	74	56.699	4.592	27.792
561	C	GLN	74	56.706	5.853	28.655
562	O	GLN	74	57.733	6.205	29.246
563	CB	GLN	74	55.438	4.607	26.937
564	CG	GLN	74	55.538	3.644	25.759
565	CD	GLN	74	56.829	3.885	24.980
566	OE1	GLN	74	57.730	3.040	25.007
567	NE2	GLN	74	56.924	5.037	24.336
568	N	GLU	75	55.709	6.690	28.427
569	CA	GLU	75	55.673	7.990	29.110
570	C	GLU	75	54.257	8.379	29.514
571	O	GLU	75	53.510	7.587	30.102
572	CB	GLU	75	56.253	9.101	28.225
573	CG	GLU	75	57.772	9.052	28.023
574	CD	GLU	75	58.150	8.215	26.800
575	OE1	GLU	75	57.252	7.925	26.017
576	OE2	GLU	75	59.327	7.934	26.630
577	N	GLN	76	53.950	9.642	29.269
578	CA	GLN	76	52.644	10.211	29.608
579	C	GLN	76	51.567	9.679	28.670
580	O	GLN	76	51.692	9.778	27.444
581	CB	GLN	76	52.706	11.737	29.491

582	CG	GLN	76	53.713	12.381	30.447
583	CD	GLN	76	55.051	12.678	29.763
584	OE1	GLN	76	55.341	12.161	28.674
585	NE2	GLN	76	55.886	13.421	30.467
586	N	ALA	77	50.454	9.272	29.259
587	CA	ALA	77	49.352	8.659	28.498
588	C	ALA	77	48.325	9.656	27.966
589	O	ALA	77	47.129	9.543	28.258
590	CB	ALA	77	48.647	7.641	29.385
591	N	ILE	78	48.783	10.610	27.174
592	CA	ILE	78	47.863	11.583	26.584
593	C	ILE	78	47.159	10.969	25.373
594	O	ILE	78	47.630	9.975	24.802
595	CB	ILE	78	48.617	12.867	26.257
596	CG1	ILE	78	49.834	12.617	25.382
597	CG2	ILE	78	49.034	13.570	27.545
598	CD1	ILE	78	50.571	13.918	25.084
599	N	LYS	79	45.944	11.438	25.134
600	CA	LYS	79	45.081	10.825	24.115
601	C	LYS	79	44.481	11.830	23.126
602	O	LYS	79	43.805	12.794	23.512
603	CB	LYS	79	43.937	10.128	24.838
604	CG	LYS	79	44.406	9.091	25.850
605	CD	LYS	79	43.212	8.464	26.555
606	CE	LYS	79	42.351	9.537	27.213
607	NZ	LYS	79	41.150	8.950	27.826
608	N	GLY	80	44.633	11.515	21.851
609	CA	GLY	80	44.036	12.335	20.784
610	C	GLY	80	43.501	11.483	19.632
611	O	GLY	80	44.212	10.640	19.078
612	N	VAL	81	42.248	11.699	19.275
613	CA	VAL	81	41.645	10.946	18.169
614	C	VAL	81	41.923	11.618	16.828
615	O	VAL	81	41.529	12.766	16.605
616	CB	VAL	81	40.139	10.838	18.392
617	CG1	VAL	81	39.428	10.202	17.201
618	CG2	VAL	81	39.835	10.047	19.656
619	N	TYR	82	42.616	10.905	15.955
620	CA	TYR	82	42.869	11.403	14.593
621	C	TYR	82	41.642	11.074	13.759
622	O	TYR	82	41.294	9.897	13.614
623	CB	TYR	82	44.077	10.717	13.952
624	CG	TYR	82	45.487	10.949	14.516
625	CD1	TYR	82	45.732	11.013	15.882
626	CD2	TYR	82	46.546	11.062	13.624
627	CE1	TYR	82	47.020	11.204	16.355
628	CE2	TYR	82	47.837	11.255	14.094
629	CZ	TYR	82	48.070	11.324	15.461
630	OH	TYR	82	49.348	11.512	15.934
631	N	SER	83	40.980	12.095	13.251
632	CA	SER	83	39.709	11.877	12.560
633	C	SER	83	39.681	12.397	11.126
634	O	SER	83	40.202	13.473	10.793
635	CB	SER	83	38.626	12.573	13.362
636	OG	SER	83	38.754	12.154	14.715
637	N	SER	84	38.979	11.633	10.307
638	CA	SER	84	38.657	12.044	8.941
639	C	SER	84	37.614	13.156	8.975
640	O	SER	84	37.138	13.562	10.045
641	CB	SER	84	38.116	10.851	8.165
642	OG	SER	84	39.118	9.845	8.164
643	N	TRP	85	37.338	13.718	7.815
644	CA	TRP	85	36.427	14.855	7.758
645	C	TRP	85	34.976	14.424	7.836
646	O	TRP	85	34.582	13.351	7.365

647	CB	TRP	85	36.711	15.752	6.550
648	CG	TRP	85	36.868	15.131	5.172
649	CD1	TRP	85	37.923	14.370	4.729
650	CD2	TRP	85	35.964	15.264	4.047
651	NE1	TRP	85	37.710	14.038	3.432
652	CE2	TRP	85	36.556	14.558	2.987
653	CE3	TRP	85	34.763	15.926	3.868
654	CZ2	TRP	85	35.916	14.509	1.754
655	CZ3	TRP	85	34.132	15.877	2.628
656	CH2	TRP	85	34.706	15.169	1.578
657	N	VAL	86	34.220	15.241	8.548
658	CA	VAL	86	32.795	15.003	8.784
659	C	VAL	86	31.962	15.331	7.540
660	O	VAL	86	31.477	16.446	7.312
661	CB	VAL	86	32.410	15.833	10.005
662	CG1	VAL	86	32.857	17.276	9.871
663	CG2	VAL	86	30.934	15.752	10.347
664	N	THR	87	31.913	14.332	6.679
665	CA	THR	87	31.179	14.425	5.422
666	C	THR	87	29.687	14.290	5.708
667	O	THR	87	29.264	13.423	6.478
668	CB	THR	87	31.674	13.310	4.495
669	OG1	THR	87	33.097	13.322	4.485
670	CG2	THR	87	31.195	13.474	3.056
671	N	ASP	88	28.901	15.089	5.003
672	CA	ASP	88	27.435	15.148	5.153
673	C	ASP	88	26.700	13.962	4.503
674	O	ASP	88	25.473	13.854	4.604
675	CB	ASP	88	27.005	16.467	4.503
676	CG	ASP	88	25.501	16.716	4.588
677	OD1	ASP	88	24.837	16.511	3.580
678	OD2	ASP	88	25.065	17.212	5.614
679	N	ASN	89	27.451	13.050	3.908
680	CA	ASN	89	26.886	11.881	3.225
681	C	ASN	89	26.010	11.001	4.126
682	O	ASN	89	26.427	10.514	5.179
683	CB	ASN	89	28.025	11.060	2.598
684	CG	ASN	89	29.028	10.431	3.582
685	OD1	ASN	89	29.207	10.861	4.730
686	ND2	ASN	89	29.677	9.388	3.093
687	N	ILE	90	24.732	10.991	3.785
688	CA	ILE	90	23.753	10.066	4.369
689	C	ILE	90	23.098	9.270	3.239
690	O	ILE	90	22.384	8.280	3.459
691	CB	ILE	90	22.734	10.894	5.156
692	CG1	ILE	90	21.559	10.056	5.653
693	CG2	ILE	90	22.253	12.084	4.333
694	CD1	ILE	90	20.503	10.892	6.367
695	N	LEU	91	23.611	9.539	2.050
696	CA	LEU	91	23.026	9.037	0.801
697	C	LEU	91	23.152	7.529	0.577
698	O	LEU	91	22.277	6.964	-0.087
699	CB	LEU	91	23.751	9.752	-0.331
700	CG	LEU	91	23.219	9.334	-1.695
701	CD1	LEU	91	21.758	9.741	-1.853
702	CD2	LEU	91	24.069	9.925	-2.811
703	N	ALA	92	24.013	6.855	1.320
704	CA	ALA	92	24.203	5.419	1.115
705	C	ALA	92	23.143	4.573	1.822
706	O	ALA	92	23.045	3.369	1.563
707	CB	ALA	92	25.588	5.058	1.618
708	N	MET	93	22.324	5.212	2.643
709	CA	MET	93	21.169	4.543	3.241
710	C	MET	93	19.932	4.726	2.359
711	O	MET	93	18.919	4.037	2.525

712	CB	MET	93	20.936	5.176	4.605
713	CG	MET	93	19.904	4.421	5.430
714	SD	MET	93	19.548	5.143	7.045
715	CE	MET	93	19.043	6.790	6.496
716	N	ALA	94	20.034	5.635	1.403
717	CA	ALA	94	18.959	5.817	0.426
718	C	ALA	94	19.291	4.973	−0.795
719	O	ALA	94	18.406	4.452	−1.485
720	CB	ALA	94	18.884	7.287	0.035
721	N	ARG	95	20.584	4.847	−1.037
722	CA	ARG	95	21.078	3.858	−1.985
723	C	ARG	95	20.910	2.497	−1.330
724	O	ARG	95	21.093	2.377	−0.115
725	CB	ARG	95	22.534	4.160	−2.316
726	CG	ARG	95	22.641	5.568	−2.884
727	CD	ARG	95	23.788	5.689	−3.879
728	NE	ARG	95	23.556	4.782	−5.017
729	CZ	ARG	95	22.886	5.121	−6.122
730	NH1	ARG	95	22.469	6.378	−6.300
731	NH2	ARG	95	22.697	4.217	−7.086
732	N	PRO	96	20.634	1.485	−2.135
733	CA	PRO	96	19.763	0.377	−1.695
734	C	PRO	96	20.355	−0.654	−0.724
735	O	PRO	96	19.710	−1.685	−0.514
736	CB	PRO	96	19.348	−0.321	−2.954
737	CG	PRO	96	20.006	0.337	−4.153
738	CD	PRO	96	20.759	1.531	−3.598
739	N	SER	97	21.524	−0.428	−0.146
740	CA	SER	97	22.109	−1.500	0.656
741	C	SER	97	23.013	−1.054	1.802
742	O	SER	97	23.704	−1.922	2.351
743	CB	SER	97	22.930	−2.386	−0.268
744	OG	SER	97	24.007	−1.596	−0.754
745	N	SER	98	23.082	0.223	2.146
746	CA	SER	98	24.019	0.556	3.226
747	C	SER	98	23.609	1.676	4.187
748	O	SER	98	22.446	1.818	4.582
749	CB	SER	98	25.400	0.793	2.622
750	OG	SER	98	25.275	1.682	1.527
751	N	GLU	99	24.631	2.341	4.700
752	CA	GLU	99	24.506	3.173	5.903
753	C	GLU	99	24.464	4.683	5.668
754	O	GLU	99	24.930	5.222	4.655
755	CB	GLU	99	25.728	2.848	6.757
756	CG	GLU	99	25.804	1.351	7.039
757	CD	GLU	99	27.232	0.924	7.370
758	OE1	GLU	99	27.830	0.307	6.500
759	OE2	GLU	99	27.578	0.974	8.541
760	N	LEU	100	23.825	5.346	6.616
761	CA	LEU	100	23.952	6.802	6.752
762	C	LEU	100	25.328	7.047	7.355
763	O	LEU	100	25.861	6.148	8.016
764	CB	LEU	100	22.856	7.388	7.649
765	CG	LEU	100	23.035	7.149	9.152
766	CD1	LEU	100	22.368	8.257	9.958
767	CD2	LEU	100	22.547	5.778	9.621
768	N	LEU	101	25.945	8.179	7.071
769	CA	LEU	101	27.336	8.312	7.496
770	C	LEU	101	27.658	9.477	8.434
771	O	LEU	101	26.914	9.821	9.364
772	CB	LEU	101	28.233	8.340	6.267
773	CG	LEU	101	29.157	7.127	6.178
774	CD1	LEU	101	30.092	7.081	7.376
775	CD2	LEU	101	28.386	5.820	6.051
776	N	GLU	102	28.772	10.116	8.124

777	CA	GLU	102	29.608	10.691	9.182
778	C	GLU	102	29.334	12.107	9.659
779	O	GLU	102	29.966	12.491	10.651
780	CB	GLU	102	31.077	10.507	8.808
781	CG	GLU	102	31.374	10.810	7.345
782	CD	GLU	102	32.824	10.443	7.033
783	OE1	GLU	102	33.377	9.651	7.786
784	OE2	GLU	102	33.352	10.968	6.062
785	N	LYS	103	28.309	12.788	9.177
786	CA	LYS	103	28.083	14.123	9.735
787	C	LYS	103	27.446	14.019	11.115
788	O	LYS	103	27.920	14.654	12.064
789	CB	LYS	103	27.207	14.984	8.839
790	CG	LYS	103	27.417	16.443	9.233
791	CD	LYS	103	26.409	17.389	8.599
792	CE	LYS	103	25.011	17.138	9.149
793	NZ	LYS	103	24.057	18.130	8.630
794	N	TYR	104	26.600	13.016	11.278
795	CA	TYR	104	25.983	12.783	12.581
796	C	TYR	104	26.847	11.854	13.428
797	O	TYR	104	26.937	12.032	14.651
798	CB	TYR	104	24.619	12.148	12.340
799	CG	TYR	104	23.863	11.778	13.610
800	CD1	TYR	104	23.700	12.715	14.624
801	CD2	TYR	104	23.323	10.505	13.743
802	CE1	TYR	104	23.019	12.370	15.783
803	CE2	TYR	104	22.642	10.158	14.902
804	CZ	TYR	104	22.499	11.090	15.922
805	OH	TYR	104	21.954	10.703	17.125
806	N	HIS	105	27.701	11.097	12.760
807	CA	HIS	105	28.493	10.095	13.471
808	C	HIS	105	29.681	10.699	14.206
809	O	HIS	105	29.883	10.316	15.364
810	CB	HIS	105	28.944	9.013	12.498
811	CG	HIS	105	27.816	8.119	12.014
812	ND1	HIS	105	27.909	7.152	11.083
813	CD2	HIS	105	26.512	8.119	12.455
814	CE1	HIS	105	26.704	6.573	10.918
815	NE2	HIS	105	25.839	7.171	11.766
816	N	ILE	106	30.159	11.847	13.745
817	CA	ILE	106	31.229	12.545	14.472
818	C	ILE	106	30.692	13.214	15.741
819	O	ILE	106	31.338	13.133	16.796
820	CB	ILE	106	31.845	13.588	13.542
821	CG1	ILE	106	32.562	12.932	12.366
822	CG2	ILE	106	32.812	14.492	14.298
823	CD1	ILE	106	33.820	12.190	12.803
824	N	ILE	107	29.409	13.544	15.720
825	CA	ILE	107	28.757	14.124	16.896
826	C	ILE	107	28.391	13.035	17.903
827	O	ILE	107	28.568	13.223	19.115
828	CB	ILE	107	27.496	14.835	16.422
829	CG1	ILE	107	27.836	15.847	15.334
830	CG2	ILE	107	26.792	15.522	17.587
831	CD1	ILE	107	26.584	16.538	14.806
832	N	ASP	108	28.180	11.833	17.390
833	CA	ASP	108	27.923	10.676	18.249
834	C	ASP	108	29.208	10.193	18.914
835	O	ASP	108	29.172	9.807	20.087
836	CB	ASP	108	27.365	9.538	17.402
837	CG	ASP	108	26.050	9.928	16.738
838	OD1	ASP	108	25.815	9.451	15.634
839	OD2	ASP	108	25.258	10.599	17.385
840	N	GLN	109	30.342	10.437	18.277
841	CA	GLN	109	31.632	10.092	18.881

842	C	GLN	109	31.991	11.082	19.984
843	O	GLN	109	32.399	10.653	21.075
844	CB	GLN	109	32.690	10.135	17.788
845	CG	GLN	109	32.379	9.125	16.692
846	CD	GLN	109	33.233	9.416	15.463
847	OE1	GLN	109	32.718	9.563	14.346
848	NE2	GLN	109	34.531	9.522	15.686
849	N	PHE	110	31.571	12.327	19.803
850	CA	PHE	110	31.764	13.353	20.834
851	C	PHE	110	31.020	12.981	22.104
852	O	PHE	110	31.659	12.752	23.142
853	CB	PHE	110	31.206	14.694	20.367
854	CG	PHE	110	31.950	15.394	19.238
855	CD1	PHE	110	31.252	16.247	18.393
856	CD2	PHE	110	33.314	15.208	19.065
857	CE1	PHE	110	31.914	16.901	17.366
858	CE2	PHE	110	33.979	15.862	18.037
859	CZ	PHE	110	33.277	16.708	17.188
860	N	LEU	111	29.754	12.635	21.938
861	CA	LEU	111	28.891	12.344	23.087
862	C	LEU	111	29.102	10.953	23.688
863	O	LEU	111	28.781	10.751	24.864
864	CB	LEU	111	27.447	12.460	22.614
865	CG	LEU	111	27.138	13.856	22.083
866	CD1	LEU	111	25.781	13.888	21.388
867	CD2	LEU	111	27.209	14.902	23.191
868	N	SER	112	29.753	10.062	22.961
869	CA	SER	112	29.974	8.709	23.478
870	C	SER	112	31.297	8.564	24.222
871	O	SER	112	31.474	7.595	24.970
872	CB	SER	112	29.958	7.730	22.309
873	OG	SER	112	31.072	8.006	21.468
874	N	HIS	113	32.216	9.496	24.029
875	CA	HIS	113	33.502	9.387	24.724
876	C	HIS	113	33.821	10.601	25.588
877	O	HIS	113	34.852	10.624	26.274
878	CB	HIS	113	34.588	9.175	23.680
879	CG	HIS	113	34.422	7.875	22.918
880	ND1	HIS	113	34.259	6.654	23.459
881	CD2	HIS	113	34.398	7.718	21.554
882	CE1	HIS	113	34.146	5.742	22.472
883	NE2	HIS	113	34.227	6.401	21.296
884	N	GLY	114	32.968	11.609	25.517
885	CA	GLY	114	33.180	12.836	26.288
886	C	GLY	114	34.321	13.619	25.659
887	O	GLY	114	35.222	14.105	26.355
888	N	ILE	115	34.289	13.676	24.339
889	CA	ILE	115	35.368	14.280	23.557
890	C	ILE	115	35.398	15.792	23.743
891	O	ILE	115	34.365	16.465	23.626
892	CB	ILE	115	35.115	13.933	22.092
893	CG1	ILE	115	35.139	12.423	21.876
894	CG2	ILE	115	36.122	14.601	21.164
895	CD1	ILE	115	36.538	11.849	22.044
896	N	LYS	116	36.582	16.316	24.018
897	CA	LYS	116	36.753	17.768	24.159
898	C	LYS	116	36.915	18.452	22.807
899	O	LYS	116	38.014	18.875	22.439
900	CB	LYS	116	37.950	18.072	25.052
901	CG	LYS	116	37.528	18.042	26.515
902	CD	LYS	116	36.401	19.047	26.742
903	CE	LYS	116	35.954	19.087	28.197
904	NZ	LYS	116	34.842	20.032	28.385
905	N	THR	117	35.771	18.654	22.162
906	CA	THR	117	35.621	19.299	20.844

907	C	THR	117	36.648	18.926	19.776
908	O	THR	117	37.519	18.053	19.938
909	CB	THR	117	35.541	20.816	21.002
910	CG1	THR	117	36.584	21.254	21.862
911	CG2	THR	117	34.221	21.237	21.635
912	N	ILE	118	36.417	19.519	18.621
913	CA	ILE	118	37.154	19.154	17.415
914	C	ILE	118	38.293	20.137	17.125
915	O	ILE	118	38.134	21.365	17.127
916	CB	ILE	118	36.111	19.041	16.300
917	CG1	ILE	118	36.394	17.862	15.387
918	CG2	ILE	118	35.967	20.316	15.472
919	CD1	ILE	118	35.199	17.607	14.475
920	N	ILE ·	119	39.479	19.570	17.023
921	CA	ILE	119	40.674	20.350	16.721
922	C	ILE	119	40.793	20.532	15.219
923	O	ILE	119	40.752	19.571	14.442
924	CB	ILE	119	41.914	19.650	17.272
925	CG1	ILE	119	41.943	19.687	18.787
926	CG2	ILE	119	43.203	20.255	16.732
927	CD1	ILE	119	43.309	19.252	19.300
928	N	ASN	120	40.887	21.793	14.849
929	CA	ASN	120	41.073	22.224	13.474
930	C	ASN	120	42.289	21.600	12.809
931	O	ASN	120	43.225	21.128	13.468
932	CB	ASN	120	41.324	23.726	13.520
933	CG	ASN	120	42.587	24.064	14.330
934	OD1	ASN	120	43.722	23.857	13.883
935	ND2	ASN	120	42.373	24.726	15.450
936	N	LEU	121	42.237	21.568	11.492
937	CA	LEU	121	43.450	21.309	10.725
938	C	LEU	121	43.658	22.383	9.669
939	O	LEU	121	44.718	23.017	9.638
940	CB	LEU	121	43.401	19.937	10.078
941	CG	LEU	121	43.758	18.834	11.061
942	CD1	LEU	121	43.749	17.491	10.352
943	CD2	LEU	121	45.124	19.094	11.686
944	N	GLN	122	42.658	22.588	8.826
945	CA	GLN	122	42.776	23.597	7.762
946	C	GLN	122	41.405	24.198	7.420
947	O	GLN	122	40.431	23.956	8.148
948	CB	GLN	122	43.472	22.918	6.571
949	CG	GLN	122	42.637	22.364	5.408
950	CD	GLN	122	41.586	21.316	5.773
951	OE1	GLN	122	40.551	21.635	6.372
952	NE2	GLN	122	41.814	20.107	5.301
953	N	ARG	123	41.383	25.111	6.459
954	CA	ARG	123	40.112	25.569	5.888
955	C	ARG	123	39.445	24.433	5.122
956	O	ARG	123	40.049	23.849	4.213
957	CB	ARG	123	40.393	26.662	4.872
958	CG	ARG	123	41.253	27.780	5.428
959	CD	ARG	123	41.601	28.783	4.336
960	NE	ARG	123	42.307	28.108	3.234
961	CZ	ARG	123	41.813	28.011	1.997
962	NH1	ARG	123	40.617	28.532	1.710
963	NH2	ARG	123	42.510	27.382	1.049
964	N	PRO	124	38.145	24.301	5.323
965	CA	PRO	124	37.364	23.270	4.624
966	C	PRO	124	37.193	23.506	3.115
967	O	PRO	124	37.145	22.529	2.352
968	CB	PRO	124	36.025	23.312	5.298
969	CG	PRO	124	35.971	24.462	6.290
970	CD	PRO	124	37.338	25.117	6.238
971	N	GLY	125	37.365	24.749	2.681

972	CA	GLY	125	37.105	25.138	1.286
973	C	GLY	125	38.355	25.187	0.405
974	O	GLY	125	38.711	26.232	-0.149
975	N	GLU	126	38.986	24.037	0.269
976	CA	GLU	126	40.101	23.843	-0.667
977	C	GLU	126	39.916	22.450	-1.249
978	O	GLU	126	40.518	21.484	-0.769
979	CB	GLU	126	41.447	23.985	0.044
980	CG	GLU	126	41.418	23.386	1.443
981	CD	GLU	126	42.827	23.187	1.989
982	OE1	GLU	126	43.143	22.054	2.330
983	OE2	GLU	126	43.529	24.172	2.170
984	N	HIS	127	39.086	22.388	-2.284
985	CA	HIS	127	38.432	21.139	-2.715
986	C	HIS	127	37.507	20.715	-1.578
987	O	HIS	127	37.160	21.537	-0.720
988	CB	HIS	127	39.428	20.020	-3.031
989	CG	HIS	127	40.524	20.386	-4.013
990	ND1	HIS	127	40.380	20.673	-5.321
991	CD2	HIS	127	41.867	20.482	-3.730
992	CE1	HIS	127	41.588	20.951	-5.853
993	NE2	HIS	127	42.507	20.833	-4.867
994	N	ALA	128	37.057	19.473	-1.596
995	CA	ALA	128	36.279	18.949	-0.457
996	C	ALA	128	37.239	18.486	0.640
997	O	ALA	128	37.448	17.284	0.848
998	CB	ALA	128	35.421	17.786	-0.938
999	N	SER	129	37.783	19.449	1.364
1000	CA	SER	129	38.948	19.170	2.196
1001	C	SER	129	38.606	18.981	3.665
1002	O	SER	129	39.463	18.541	4.443
1003	CB	SER	129	39.899	20.341	2.036
1004	OG	SER	129	41.207	19.906	2.364
1005	N	CYS	130	37.383	19.319	4.035
1006	CA	CYS	130	36.922	19.121	5.411
1007	C	CYS	130	35.443	19.471	5.489
1008	O	CYS	130	35.022	20.499	4.954
1009	CB	CYS	130	37.717	20.028	6.350
1010	SG	CYS	130	37.778	19.479	8.067
1011	N	GLY	131	34.661	18.613	6.116
1012	CA	GLY	131	33.228	18.891	6.272
1013	C	GLY	131	32.962	19.833	7.445
1014	O	GLY	131	33.828	20.030	8.306
1015	N	ASN	132	31.771	20.409	7.462
1016	CA	ASN	132	31.397	21.326	8.548
1017	C	ASN	132	30.022	21.008	9.141
1018	O	ASN	132	28.984	21.206	8.499
1019	CB	ASN	132	31.402	22.761	8.028
1020	CG	ASN	132	30.993	23.686	9.170
1021	OD1	ASN	132	31.421	23.490	10.313
1022	ND2	ASN	132	30.109	24.621	8.876
1023	N	PRO	133	30.034	20.467	10.351
1024	CA	PRO	133	28.805	20.288	11.135
1025	C	PRO	133	28.365	21.525	11.944
1026	O	PRO	133	27.252	21.530	12.484
1027	CB	PRO	133	29.169	19.190	12.086
1028	CG	PRO	133	30.689	19.125	12.189
1029	CD	PRO	133	31.220	20.045	11.100
1030	N	LEU	134	29.197	22.552	12.020
1031	CA	LEU	134	28.928	23.682	12.914
1032	C	LEU	134	28.041	24.744	12.279
1033	O	LEU	134	28.259	25.185	11.141
1034	CB	LEU	134	30.260	24.310	13.315
1035	CG	LEU	134	31.145	23.316	14.065
1036	CD1	LEU	134	32.514	23.914	14.370

1037	CD2	LEU	134	30.473	22.846	15.350
1038	N	GLU	135	27.052	25.166	13.048
1039	CA	GLU	135	26.172	26.258	12.626
1040	C	GLU	135	26.925	27.581	12.758
1041	O	GLU	135	27.237	28.036	13.864
1042	CB	GLU	135	24.932	26.225	13.514
1043	CG	GLU	135	23.821	27.140	13.016
1044	CD	GLU	135	22.549	26.877	13.820
1045	OE1	GLU	135	22.673	26.118	14.775
1046	OE2	GLU	135	21.489	27.082	13.244
1047	N	GLN	136	27.229	28.168	11.611
1048	CA	GLN	136	28.077	29.366	11.560
1049	C	GLN	136	27.301	30.640	11.864
1050	O	GLN	136	27.862	31.618	12.369
1051	CB	GLN	136	28.643	29.459	10.150
1052	CG	GLN	136	29.423	28.203	9.787
1053	CD	GLN	136	29.725	28.195	8.293
1054	OE1	GLN	136	29.167	27.387	7.541
1055	NE2	GLN	136	30.573	29.120	7.877
1056	N	GLU	137	26.014	30.614	11.574
1057	CA	GLU	137	25.150	31.722	11.974
1058	C	GLU	137	24.177	31.221	13.030
1059	O	GLU	137	23.581	30.149	12.864
1060	CB	GLU	137	24.418	32.291	10.762
1061	CG	GLU	137	23.632	31.233	10.000
1062	CD	GLU	137	22.867	31.887	8.855
1063	OE1	GLU	137	22.781	31.265	7.805
1064	OE2	GLU	137	22.472	33.032	9.020
1065	N	SER	138	24.060	31.986	14.104
1066	CA	SER	138	23.226	31.604	15.250
1067	C	SER	138	23.669	30.259	15.822
1068	O	SER	138	23.109	29.207	15.490
1069	CB	SER	138	21.759	31.541	14.830
1070	OG	SER	138	21.003	31.101	15.948
1071	N	GLY	139	24.724	30.304	16.614
1072	CA	GLY	139	25.233	29.096	17.258
1073	C	GLY	139	25.932	29.478	18.553
1074	O	GLY	139	25.311	30.001	19.485
1075	N	PHE	140	27.227	29.235	18.587
1076	CA	PHE	140	28.023	29.597	19.759
1077	C	PHE	140	28.840	30.846	19.478
1078	O	PHE	140	28.592	31.552	18.495
1079	CB	PHE	140	28.918	28.428	20.147
1080	CG	PHE	140	28.135	27.244	20.707
1081	CD1	PHE	140	27.682	27.283	22.019
1082	CD2	PHE	140	27.860	26.139	19.910
1083	CE1	PHE	140	26.966	26.212	22.539
1084	CE2	PHE	140	27.144	25.069	20.430
1085	CZ	PHE	140	26.699	25.104	21.745
1086	N	THR	141	29.746	31.146	20.391
1087	CA	THR	141	30.615	32.321	20.264
1088	C	THR	141	31.653	32.097	19.162
1089	O	THR	141	31.853	30.956	18.731
1090	CB	THR	141	31.286	32.549	21.615
1091	OG1	THR	141	31.941	33.806	21.601
1092	CG2	THR	141	32.300	31.460	21.949
1093	N	TYR	142	32.113	33.186	18.565
1094	CA	TYR	142	33.120	33.121	17.492
1095	C	TYR	142	34.209	34.181	17.682
1096	O	TYR	142	33.982	35.362	17.393
1097	CB	TYR	142	32.444	33.394	16.145
1098	CG	TYR	142	31.164	32.611	15.854
1099	CD1	TYR	142	29.955	33.292	15.775
1100	CD2	TYR	142	31.204	31.238	15.644
1101	CE1	TYR	142	28.781	32.597	15.517

1102	CE2	TYR	142	30.029	30.541	15.388
1103	CZ	TYR	142	28.821	31.223	15.331
1104	OH	TYR	142	27.647	30.531	15.136
1105	N	LEU	143	35.382	33.759	18.123
1106	CA	LEU	143	36.538	34.667	18.266
1107	C	LEU	143	37.080	35.096	16.903
1108	O	LEU	143	37.544	34.255	16.125
1109	CB	LEU	143	37.626	33.929	19.044
1110	CG	LEU	143	38.909	34.741	19.216
1111	CD1	LEU	143	38.692	35.937	20.135
1112	CD2	LEU	143	40.028	33.864	19.764
1113	N	PRO	144	37.040	36.395	16.638
1114	CA	PRO	144	37.290	36.941	15.294
1115	C	PRO	144	38.764	37.165	14.918
1116	O	PRO	144	39.135	38.289	14.563
1117	CB	PRO	144	36.570	38.254	15.289
1118	CG	PRO	144	36.205	38.629	16.718
1119	CD	PRO	144	36.580	37.430	17.569
1120	N	GLU	145	39.605	36.149	15.032
1121	CA	GLU	145	40.963	36.277	14.489
1122	C	GLU	145	40.975	35.718	13.074
1123	O	GLU	145	40.394	34.654	12.829
1124	CB	GLU	145	41.981	35.541	15.345
1125	CG	GLU	145	42.179	36.208	16.698
1126	CD	GLU	145	43.285	35.485	17.462
1127	OE1	GLU	145	44.016	34.732	16.832
1128	OE2	GLU	145	43.291	35.596	18.681
1129	N	ALA	146	41.745	36.358	12.205
1130	CA	ALA	146	41.772	36.020	10.769
1131	C	ALA	146	41.935	34.533	10.483
1132	O	ALA	146	40.993	33.877	10.028
1133	CB	ALA	146	42.932	36.756	10.123
1134	N	PHE	147	43.069	33.979	10.873
1135	CA	PHE	147	43.301	32.550	10.640
1136	C	PHE	147	42.961	31.685	11.856
1137	O	PHE	147	43.265	30.485	11.846
1138	CB	PHE	147	44.743	32.302	10.203
1139	CG	PHE	147	45.104	32.760	8.783
1140	CD1	PHE	147	44.119	33.164	7.890
1141	CD2	PHE	147	46.434	32.753	8.382
1142	CE1	PHE	147	44.463	33.575	6.609
1143	CE2	PHE	147	46.780	33.163	7.101
1144	CZ	PHE	147	45.795	33.577	6.215
1145	N	MET	148	42.316	32.267	12.857
1146	CA	MET	148	42.010	31.551	14.106
1147	C	MET	148	40.652	31.969	14.670
1148	O	MET	148	40.578	32.723	15.652
1149	CB	MET	148	43.081	31.840	15.157
1150	CG	MET	148	44.417	31.178	14.841
1151	SD	MET	148	45.728	31.446	16.054
1152	CE	MET	148	47.004	30.406	15.307
1153	N	GLU	149	39.594	31.418	14.102
1154	CA	GLU	149	38.246	31.738	14.593
1155	C	GLU	149	37.769	30.699	15.601
1156	O	GLU	149	37.243	29.646	15.223
1157	CB	GLU	149	37.257	31.790	13.435
1158	CG	GLU	149	35.869	32.194	13.924
1159	CD	GLU	149	34.845	32.048	12.803
1160	OE1	GLU	149	33.686	31.814	13.118
1161	OE2	GLU	149	35.250	32.129	11.652
1162	N	ALA	150	37.921	31.009	16.875
1163	CA	ALA	150	37.520	30.058	17.921
1164	C	ALA	150	36.026	30.099	18.231
1165	O	ALA	150	35.539	31.038	18.872
1166	CB	ALA	150	38.307	30.354	19.192

1167	N	GLY	151	35.325	29.061	17.810
1168	CA	GLY	151	33.903	28.917	18.129
1169	C	GLY	151	33.774	28.180	19.456
1170	O	GLY	151	34.010	28.752	20.529
1171	N	ILE	152	33.405	26.911	19.373
1172	CA	ILE	152	33.506	26.032	20.544
1173	C	ILE	152	34.898	25.412	20.573
1174	O	ILE	152	35.379	24.937	21.608
1175	CB	ILE	152	32.429	24.951	20.513
1176	CG1	ILE	152	32.175	24.424	19.105
1177	CG2	ILE	152	31.146	25.457	21.154
1178	CD1	ILE	152	31.091	23.354	19.103
1179	N	TYR	153	35.500	25.380	19.396
1180	CA	TYR	153	36.934	25.163	19.253
1181	C	TYR	153	37.399	25.983	18.059
1182	O	TYR	153	36.591	26.481	17.266
1183	CB	TYR	153	37.281	23.689	19.105
1184	CG	TYR	153	38.254	23.211	20.184
1185	CD1	TYR	153	38.314	23.882	21.401
1186	CD2	TYR	153	39.080	22.118	19.957
1187	CE1	TYR	153	39.184	23.452	22.393
1188	CE2	TYR	153	39.952	21.687	20.948
1189	CZ	TYR	153	40.001	22.353	22.164
1190	OH	TYR	153	40.847	21.907	23.155
1191	N	PHE	154	38.697	26.194	18.010
1192	CA	PHE	154	39.306	27.134	17.065
1193	C	PHE	154	39.332	26.579	15.648
1194	O	PHE	154	39.605	25.390	15.453
1195	CB	PHE	154	40.737	27.401	17.532
1196	CG	PHE	154	41.024	26.975	18.976
1197	CD1	PHE	154	40.623	27.774	20.041
1198	CD2	PHE	154	41.705	25.787	19.219
1199	CE1	PHE	154	40.861	27.363	21.345
1200	CE2	PHE	154	41.946	25.379	20.523
1201	CZ	PHE	154	41.517	26.163	21.585
1202	N	TYR	155	38.948	27.412	14.696
1203	CA	TYR	155	39.098	27.093	13.273
1204	C	TYR	155	40.399	27.642	12.704
1205	O	TYR	155	40.728	28.823	12.878
1206	CB	TYR	155	37.925	27.670	12.498
1207	CG	TYR	155	36.878	26.626	12.143
1208	CD1	TYR	155	35.532	26.965	12.087
1209	CD2	TYR	155	37.283	25.325	11.871
1210	CE1	TYR	155	34.589	26.000	11.757
1211	CE2	TYR	155	36.343	24.360	11.541
1212	CZ	TYR	155	34.998	24.701	11.485
1213	OH	TYR	155	34.069	23.738	11.166
1214	N	ASN	156	41.072	26.784	11.958
1215	CA	ASN	156	42.381	27.092	11.379
1216	C	ASN	156	42.226	27.502	9.928
1217	O	ASN	156	41.957	26.676	9.053
1218	CB	ASN	156	43.217	25.821	11.428
1219	CG	ASN	156	44.698	26.066	11.163
1220	OD1	ASN	156	45.090	26.814	10.255
1221	ND2	ASN	156	45.506	25.410	11.975
1222	N	PHE	157	42.505	28.760	9.663
1223	CA	PHE	157	42.413	29.259	8.294
1224	C	PHE	157	43.786	29.501	7.672
1225	O	PHE	157	43.881	30.120	6.605
1226	CB	PHE	157	41.580	30.534	8.279
1227	CG	PHE	157	40.146	30.340	8.764
1228	CD1	PHE	157	39.321	29.410	8.144
1229	CD2	PHE	157	39.666	31.095	9.825
1230	CE1	PHE	157	38.016	29.235	8.586
1231	CE2	PHE	157	38.361	30.922	10.265

1232	CZ	PHE	157	37.536	29.992	9.646
1233	N	GLY	158	44.832	28.999	8.307
1234	CA	GLY	158	46.189	29.294	7.843
1235	C	GLY	158	46.902	28.091	7.240
1236	O	GLY	158	47.685	28.239	6.293
1237	N	TRP	159	46.672	26.924	7.814
1238	CA	TRP	159	47.369	25.725	7.348
1239	C	TRP	159	46.776	25.224	6.033
1240	O	TRP	159	45.568	24.991	5.916
1241	CB	TRP	159	47.249	24.653	8.424
1242	CG	TRP	159	48.486	23.794	8.580
1243	CD1	TRP	159	49.470	23.579	7.641
1244	CD2	TRP	159	48.873	23.051	9.756
1245	NE1	TRP	159	50.408	22.760	8.179
1246	CE2	TRP	159	50.094	22.428	9.445
1247	CE3	TRP	159	48.300	22.881	11.006
1248	CZ2	TRP	159	50.731	21.642	10.396
1249	CZ3	TRP	159	48.942	22.092	11.952
1250	CH2	TRP	159	50.152	21.475	11.649
1251	N	LYS	160	47.624	25.195	5.021
1252	CA	LYS	160	47.244	24.638	3.723
1253	C	LYS	160	47.419	23.122	3.765
1254	O	LYS	160	48.291	22.620	4.488
1255	CB	LYS	160	48.167	25.248	2.669
1256	CG	LYS	160	47.720	24.950	1.238
1257	CD	LYS	160	48.755	25.330	0.179
1258	CE	LYS	160	49.780	24.225	−0.106
1259	NZ	LYS	160	50.743	24.013	0.988
1260	N	ASP	161	46.556	22.404	3.060
1261	CA	ASP	161	46.691	20.945	2.953
1262	C	ASP	161	48.086	20.566	2.463
1263	O	ASP	161	48.620	21.144	1.507
1264	CB	ASP	161	45.627	20.370	2.014
1265	CG	ASP	161	45.747	20.900	0.582
1266	OD1	ASP	161	45.211	21.967	0.311
1267	OD2	ASP	161	46.358	20.212	−0.223
1268	N	TYR	162	48.697	19.685	3.240
1269	CA	TYR	162	50.052	19.168	3.003
1270	C	TYR	162	51.103	20.280	2.954
1271	O	TYR	162	51.941	20.310	2.046
1272	CB	TYR	162	50.059	18.374	1.697
1273	CG	TYR	162	49.043	17.233	1.651
1274	CD1	TYR	162	49.079	16.226	2.609
1275	CD2	TYR	162	48.082	17.204	0.647
1276	CE1	TYR	162	48.150	15.194	2.566
1277	CE2	TYR	162	47.153	16.172	0.603
1278	CZ	TYR	162	47.190	15.170	1.564
1279	OH	TYR	162	46.267	14.147	1.522
1280	N	GLY	163	51.052	21.184	3.919
1281	CA	GLY	163	52.056	22.251	3.988
1282	C	GLY	163	52.548	22.471	5.412
1283	O	GLY	163	52.355	21.627	6.297
1284	N	VAL	164	53.243	23.577	5.615
1285	CA	VAL	164	53.727	23.930	6.957
1286	C	VAL	164	53.446	25.394	7.294
1287	O	VAL	164	53.652	26.294	6.472
1288	CB	VAL	164	55.226	23.647	7.064
1289	CG1	VAL	164	55.522	22.159	7.235
1290	CG2	VAL	164	56.004	24.230	5.888
1291	N	ALA	165	52.895	25.602	8.477
1292	CA	ALA	165	52.682	26.960	8.987
1293	C	ALA	165	53.917	27.413	9.763
1294	O	ALA	165	54.829	26.612	10.000
1295	CB	ALA	165	51.446	26.974	9.880
1296	N	SER	166	53.981	28.696	10.081

1297	CA	SER	166	55.134	29.222	10.827
1298	C	SER	166	55.206	28.591	12.210
1299	O	SER	166	54.179	28.208	12.787
1300	CB	SER	166	55.016	30.733	11.008
1301	OG	SER	166	54.381	30.978	12.260
1302	N	LEU	167	56.401	28.624	12.777
1303	CA	LEU	167	56.646	28.091	14.124
1304	C	LEU	167	55.706	28.734	15.133
1305	O	LEU	167	54.831	28.050	15.675
1306	CB	LEU	167	58.081	28.394	14.575
1307	CG	LEU	167	59.173	28.487	14.000
1308	CD1	LEU	167	59.566	27.847	12.568
1309	CD2	LEU	167	60.417	27.574	14.877
1310	N	THR	168	55.665	30.056	15.110
1311	CA	THR	168	54.860	30.796	16.086
1312	C	THR	168	53.347	30.667	15.887
1313	O	THR	168	52.653	30.557	16.905
1314	CB	THR	168	55.270	32.261	16.033
1315	OG1	THR	168	54.985	32.775	14.736
1316	CG2	THR	168	56.764	32.402	16.293
1317	N	THR	169	52.866	30.447	14.668
1318	CA	THR	169	51.425	30.226	14.487
1319	C	THR	169	50.988	28.809	14.853
1320	O	THR	169	49.834	28.611	15.248
1321	CB	THR	169	51.041	30.496	13.036
1322	OG1	THR	169	51.736	29.580	12.202
1323	CG2	THR	169	51.404	31.909	12.603
1324	N	ILE	170	51.907	27.860	14.871
1325	CA	ILE	170	51.524	26.527	15.321
1326	C	ILE	170	51.658	26.442	16.834
1327	O	ILE	170	50.764	25.907	17.503
1328	CB	ILE	170	52.425	25.484	14.670
1329	CG1	ILE	170	52.401	25.606	13.152
1330	CG2	ILE	170	51.985	24.083	15.080
1331	CD1	ILE	170	53.336	24.592	12.503
1332	N	LEU	171	52.593	27.206	17.374
1333	CA	LEU	171	52.840	27.147	18.816
1334	C	LEU	171	51.840	27.976	19.612
1335	O	LEU	171	51.397	27.517	20.672
1336	CB	LEU	171	54.261	27.611	19.105
1337	CG	LEU	171	55.280	26.719	18.403
1338	CD1	LEU	171	56.698	27.206	18.659
1339	CD2	LEU	171	55.126	25.258	18.811
1340	N	ASP	172	51.303	29.033	19.023
1341	CA	ASP	172	50.250	29.760	19.736
1342	C	ASP	172	48.896	29.081	19.525
1343	O	ASP	172	48.082	29.077	20.455
1344	CB	ASP	172	50.214	31.248	19.350
1345	CG	ASP	172	49.557	31.556	18.001
1346	OD1	ASP	172	49.834	30.852	17.044
1347	OD2	ASP	172	48.884	32.576	17.929
1348	N	MET	173	48.792	28.266	18.484
1349	CA	MET	173	47.564	27.508	18.254
1350	C	MET	173	47.456	26.354	19.245
1351	O	MET	173	46.462	26.274	19.980
1352	CB	MET	173	47.595	26.952	16.833
1353	CG	MET	173	46.286	26.292	16.397
1354	SD	MET	173	44.923	27.378	15.898
1355	CE	MET	173	44.327	27.971	17.498
1356	N	VAL	174	48.568	25.667	19.470
1357	CA	VAL	174	48.554	24.541	20.410
1358	C	VAL	174	48.621	24.973	21.875
1359	O	VAL	174	48.155	24.217	22.733
1360	CB	VAL	174	49.698	23.575	20.103
1361	CG1	VAL	174	49.528	22.933	18.735

1362	CG2	VAL	174	51.070	24.225	20.219
1363	N	LYS	175	48.941	26.231	22.137
1364	CA	LYS	175	48.966	26.709	23.520
1365	C	LYS	175	47.573	27.157	23.972
1366	O	LYS	175	47.325	27.310	25.173
1367	CB	LYS	175	49.966	27.858	23.613
1368	CG	LYS	175	50.843	27.759	24.861
1369	CD	LYS	175	50.068	28.004	26.150
1370	CE	LYS	175	50.857	27.559	27.372
1371	NZ	LYS	175	51.160	26.121	27.291
1372	N	VAL	176	46.641	27.274	23.040
1373	CA	VAL	176	45.268	27.575	23.441
1374	C	VAL	176	44.443	26.286	23.556
1375	O	VAL	176	43.335	26.301	24.110
1376	CB	VAL	176	44.659	28.544	22.428
1377	CG1	VAL	176	43.342	29.119	22.938
1378	CG2	VAL	176	45.615	29.697	22.155
1379	N	MET	177	45.023	25.166	23.148
1380	CA	MET	177	44.303	23.887	23.195
1381	C	MET	177	44.238	23.299	24.602
1382	O	MET	177	45.236	22.830	25.161
1383	CB	MET	177	44.991	22.893	22.268
1384	CG	MET	177	44.920	23.350	20.817
1385	SD	MET	177	45.681	22.240	19.613
1386	CE	MET	177	45.300	23.164	18.107
1387	N	THR	178	43.034	23.311	25.148
1388	CA	THR	178	42.785	22.687	26.449
1389	C	THR	178	42.695	21.175	26.275
1390	O	THR	178	41.769	20.664	25.637
1391	CB	THR	178	41.473	23.232	27.004
1392	OG1	THR	178	41.603	24.643	27.118
1393	CG2	THR	178	41.161	22.671	28.388
1394	N	PHE	179	43.670	20.476	26.832
1395	CA	PHE	179	43.723	19.020	26.675
1396	C	PHE	179	42.899	18.305	27.744
1397	O	PHE	179	42.239	17.305	27.441
1398	CB	PHE	179	45.182	18.599	26.783
1399	CG	PHE	179	45.605	17.563	25.750
1400	CD1	PHE	179	45.058	17.599	24.474
1401	CD2	PHE	179	46.546	16.595	26.074
1402	CE1	PHE	179	45.446	16.663	23.524
1403	CE2	PHE	179	46.933	15.660	25.124
1404	CZ	PHE	179	46.384	15.693	23.849
1405	N	ALA	180	42.832	18.924	28.917
1406	CA	ALA	180	42.058	18.435	30.076
1407	C	ALA	180	42.026	16.914	30.225
1408	O	ALA	180	41.072	16.267	29.774
1409	CB	ALA	180	40.634	18.967	29.962
1410	N	LEU	181	42.892	16.407	31.091
1411	CA	LEU	181	43.068	14.951	31.266
1412	C	LEU	181	42.018	14.314	32.199
1413	O	LEU	181	42.150	13.159	32.618
1414	CB	LEU	181	44.482	14.717	31.797
1415	CG	LEU	181	44.962	13.284	31.576
1416	CD1	LEU	181	44.904	12.909	30.099
1417	CD2	LEU	181	46.370	13.084	32.128
1418	N	GLN	182	41.006	15.088	32.558
1419	CA	GLN	182	39.898	14.583	33.363
1420	C	GLN	182	38.719	14.224	32.460
1421	O	GLN	182	37.697	13.711	32.931
1422	CB	GLN	182	39.495	15.690	34.327
1423	CG	GLN	182	40.682	16.109	35.188
1424	CD	GLN	182	40.349	17.383	35.956
1425	OE1	GLN	182	39.583	18.225	35.476
1426	NE2	GLN	182	40.996	17.549	37.096

1427	N	GLU	183	38.840	14.551	31.183
1428	CA	GLU	183	37.771	14.260	30.223
1429	C	GLU	183	38.265	13.284	29.161
1430	O	GLU	183	39.333	12.679	29.312
1431	CB	GLU	183	37.271	15.551	29.572
1432	CG	GLU	183	36.287	16.343	30.444
1433	CD	GLU	183	36.963	17.180	31.533
1434	OE1	GLU	183	36.262	17.593	32.444
1435	OE2	GLU	183	38.143	17.472	31.381
1436	N	GLY	184	37.472	13.111	28.118
1437	CA	GLY	184	37.827	12.176	27.051
1438	C	GLY	184	38.821	12.792	26.077
1439	O	GLY	184	39.341	13.897	26.285
1440	N	LYS	185	39.074	12.052	25.013
1441	CA	LYS	185	40.052	12.451	23.992
1442	C	LYS	185	39.645	13.740	23.291
1443	O	LYS	185	38.475	14.140	23.312
1444	CB	LYS	185	40.179	11.368	22.916
1445	CG	LYS	185	40.876	10.079	23.355
1446	CD	LYS	185	39.952	9.039	23.985
1447	CE	LYS	185	38.873	8.586	23.011
1448	NZ	LYS	185	38.014	7.560	23.620
1449	N	VAL	186	40.632	14.439	22.766
1450	CA	VAL	186	40.337	15.581	21.896
1451	C	VAL	186	40.268	15.048	20.459
1452	O	VAL	186	40.880	14.009	20.180
1453	CB	VAL	186	41.444	16.611	22.095
1454	CG1	VAL	186	42.714	16.224	21.343
1455	CG2	VAL	186	40.986	18.009	21.701
1456	N	ALA	187	39.449	15.633	19.599
1457	CA	ALA	187	39.310	15.068	18.244
1458	C	ALA	187	39.915	15.942	17.149
1459	O	ALA	187	39.243	16.836	16.633
1460	CB	ALA	187	37.830	14.857	17.952
1461	N	ILE	188	41.104	15.583	16.700
1462	CA	ILE	188	41.822	16.361	15.679
1463	C	ILE	188	41.389	15.903	14.292
1464	O	ILE	188	41.661	14.757	13.916
1465	CB	ILE	188	43.303	16.068	15.867
1466	CG1	ILE	188	43.645	16.132	17.346
1467	CG2	ILE	188	44.165	17.048	15.077
1468	CD1	ILE	188	45.105	15.801	17.583
1469	N	HIS	189	40.809	16.793	13.511
1470	CA	HIS	189	40.123	16.322	12.310
1471	C	HIS	189	40.218	17.235	11.076
1472	O	HIS	189	40.412	18.452	11.201
1473	CB	HIS	189	38.666	16.150	12.734
1474	CG	HIS	189	37.645	16.907	11.916
1475	ND1	HIS	189	36.854	16.388	10.962
1476	CD2	HIS	189	37.343	18.245	12.007
1477	CE1	HIS	189	36.081	17.366	10.449
1478	NE2	HIS	189	36.380	18.512	11.098
1479	N	CYS	190	40.267	16.579	9.918
1480	CA	CYS	190	39.981	17.179	8.591
1481	C	CYS	190	40.238	16.212	7.439
1482	O	CYS	190	39.808	15.059	7.500
1483	CB	CYS	190	40.651	18.521	8.306
1484	SG	CYS	190	39.629	19.964	8.719
1485	N	HIS	191	41.024	16.646	6.462
1486	CA	HIS	191	41.066	16.005	5.128
1487	C	HIS	191	41.406	14.514	5.072
1488	O	HIS	191	40.917	13.830	4.165
1489	CB	HIS	191	42.094	16.759	4.301
1490	CG	HIS	191	41.915	16.692	2.796
1491	ND1	HIS	191	40.837	16.247	2.123

1492	CD2	HIS	191	42.834	17.096	1.856
1493	CE1	HIS	191	41.058	16.361	0.796
1494	NE2	HIS	191	42.293	16.888	0.633
1495	N	ALA	192	42.169	14.000	6.020
1496	CA	ALA	192	42.425	12.564	6.015
1497	C	ALA	192	42.543	11.995	7.425
1498	O	ALA	192	41.792	11.092	7.814
1499	CB	ALA	192	43.710	12.303	5.240
1500	N	GLY	193	43.521	12.502	8.155
1501	CA	GLY	193	43.855	11.952	9.468
1502	C	GLY	193	45.374	11.866	9.584
1503	O	GLY	193	45.935	11.748	10.677
1504	N	LEU	194	46.025	11.919	8.436
1505	CA	LEU	194	47.486	11.976	8.389
1506	C	LEU	194	47.978	13.408	8.189
1507	O	LEU	194	47.199	14.364	8.323
1508	CB	LEU	194	47.962	11.051	7.272
1509	CG	LEU	194	47.154	11.149	5.974
1510	CD1	LEU	194	47.563	12.342	5.111
1511	CD2	LEU	194	47.327	9.872	5.163
1512	N	GLY	195	49.288	13.538	8.046
1513	CA	GLY	195	49.927	14.801	7.650
1514	C	GLY	195	49.977	15.824	8.774
1515	O	GLY	195	50.637	15.643	9.806
1516	N	ARG	196	49.081	16.787	8.646
1517	CA	ARG	196	48.978	17.886	9.603
1518	C	ARG	196	48.322	17.443	10.904
1519	O	ARG	196	48.654	18.000	11.955
1520	CB	ARG	196	48.128	18.967	8.956
1521	CG	ARG	196	48.810	19.526	7.717
1522	CD	ARG	196	47.793	20.137	6.766
1523	NE	ARG	196	46.986	19.058	6.181
1524	CZ	ARG	196	45.667	18.928	6.324
1525	NH1	ARG	196	44.983	19.818	7.043
1526	NH2	ARG	196	45.036	17.897	5.764
1527	N	THR	197	47.639	16.307	10.874
1528	CA	THR	197	47.051	15.770	12.106
1529	C	THR	197	48.178	15.219	12.966
1530	O	THR	197	48.372	15.661	14.108
1531	CB	THR	197	46.113	14.611	11.787
1532	OG1	THR	197	45.332	14.898	10.637
1533	CG2	THR	197	45.181	14.306	12.952
1534	N	GLY	198	49.064	14.504	12.286
1535	CA	GLY	198	50.254	13.915	12.899
1536	C	GLY	198	51.148	14.995	13.489
1537	O	GLY	198	51.301	15.042	14.716
1538	N	VAL	199	51.495	15.978	12.671
1539	CA	VAL	199	52.389	17.064	13.107
1540	C	VAL	199	51.831	17.887	14.267
1541	O	VAL	199	52.541	18.074	15.263
1542	CB	VAL	199	52.607	18.018	11.935
1543	CG1	VAL	199	53.525	19.175	12.315
1544	CG2	VAL	199	53.162	17.298	10.718
1545	N	LEU	200	50.535	18.156	14.250
1546	CA	LEU	200	49.937	19.032	15.260
1547	C	LEU	200	49.958	18.397	16.646
1548	O	LEU	200	50.546	18.976	17.572
1549	CB	LEU	200	48.501	19.308	14.833
1550	CG	LEU	200	47.866	20.429	15.646
1551	CD1	LEU	200	48.671	21.714	15.513
1552	CD2	LEU	200	46.431	20.658	15.191
1553	N	ILE	201	49.574	17.133	16.725
1554	CA	ILE	201	49.565	16.485	18.038
1555	C	ILE	201	50.939	15.940	18.416
1556	O	ILE	201	51.251	15.910	19.609

1557	CB	ILE	201	48.522	15.371	18.065
1558	CG1	ILE	201	48.510	14.636	19.395
1559	CG2	ILE	201	48.747	14.392	16.921
1560	CD1	ILE	201	47.526	13.469	19.398
1561	N	ALA	200	51.836	15.794	17.458
1562	CA	ALA	200	53.167	15.313	17.798
1563	C	ALA	200	54.113	16.437	18.228
1564	O	ALA	200	55.036	16.173	19.012
1565	CB	ALA	200	53.716	14.528	16.615
1566	N	CYS	203	53.768	17.681	17.924
1567	CA	CYS	203	54.506	18.803	18.522
1568	C	CYS	203	54.186	18.848	20.008
1569	O	CYS	203	55.092	18.732	20.846
1570	CB	CYS	203	54.044	20.150	17.965
1571	SG	CYS	203	54.255	20.541	16.215
1572	N	TYR	204	52.901	18.691	20.289
1573	CA	TYR	204	52.381	18.790	21.653
1574	C	TYR	204	52.749	17.561	22.485
1575	O	TYR	204	53.101	17.701	23.662
1576	CB	TYR	204	50.864	18.893	21.507
1577	CG	TYR	204	50.116	19.555	22.660
1578	CD1	TYR	204	50.148	20.938	22.789
1579	CD2	TYR	204	49.398	18.789	23.569
1580	CE1	TYR	204	49.449	21.556	23.815
1581	CE2	TYR	204	48.698	19.407	24.596
1582	CZ	TYR	204	48.717	20.790	24.711
1583	OH	TYR	204	47.900	21.415	25.632
1584	N	LEU	205	52.906	16.431	21.818
1585	CA	LEU	205	53.356	15.200	22.469
1586	C	LEU	205	54.809	15.287	22.905
1587	O	LEU	205	55.090	15.078	24.090
1588	CB	LEU	205	53.221	14.057	21.469
1589	CG	LEU	205	53.947	12.800	21.938
1590	CD1	LEU	205	53.322	12.211	23.199
1591	CD2	LEU	205	53.993	11.765	20.824
1592	N	VAL	206	55.672	15.817	22.055
1593	CA	VAL	206	57.088	15.847	22.410
1594	C	VAL	206	57.393	16.985	23.378
1595	O	VAL	206	58.169	16.766	24.318
1596	CB	VAL	206	57.900	15.968	21.131
1597	CG1	VAL	206	59.388	16.041	21.436
1598	CG2	VAL	206	57.610	14.782	20.220
1599	N	PHE	207	56.547	18.003	23.359
1600	CA	PHE	207	56.645	19.108	24.318
1601	C	PHE	207	56.094	18.744	25.700
1602	O	PHE	207	56.551	19.302	26.705
1603	CB	PHE	207	55.851	20.278	23.739
1604	CG	PHE	207	55.550	21.412	24.716
1605	CD1	PHE	207	54.280	21.522	25.271
1606	CD2	PHE	207	56.532	22.338	25.041
1607	CE1	PHE	207	53.997	22.549	26.162
1608	CE2	PHE	207	56.247	23.366	25.930
1609	CZ	PHE	207	54.981	23.470	26.492
1610	N	ALA	208	55.203	17.768	25.765
1611	CA	ALA	208	54.683	17.326	27.059
1612	C	ALA	208	55.512	16.177	27.620
1613	O	ALA	208	55.587	15.994	28.842
1614	CB	ALA	208	53.240	16.870	26.879
1615	N	THR	209	56.200	15.477	26.734
1616	CA	THR	209	57.076	14.388	27.154
1617	C	THR	209	58.424	14.948	27.589
1618	O	THR	209	58.584	15.171	28.799
1619	CB	THR	209	57.205	13.376	26.017
1620	OG1	THR	209	55.894	12.910	25.726
1621	CG2	THR	209	58.034	12.158	26.414

1622	N	ARG	210	59.269	15.261	26.607
1623	CA	ARG	210	60.654	15.787	26.732
1624	C	ARG	210	61.591	15.051	25.762
1625	O	ARG	210	62.702	15.514	25.476
1626	CB	ARG	210	61.214	15.596	28.142
1627	CG	ARG	210	62.513	16.344	28.397
1628	CD	ARG	210	63.009	16.054	29.806
1629	NE	ARG	210	63.160	14.602	29.997
1630	CZ	ARG	210	64.308	14.029	30.363
1631	NH1	ARG	210	64.399	12.699	30.423
1632	NH2	ARG	210	65.386	14.783	30.593
1633	N	MET	211	61.107	13.959	25.191
1634	CA	MET	211	62.011	13.028	24.496
1635	C	MET	211	61.987	13.101	22.970
1636	O	MET	211	61.642	14.125	22.372
1637	CB	MET	211	61.716	11.610	24.965
1638	CG	MET	211	62.045	11.464	26.447
1639	SD	MET	211	61.917	9.793	27.118
1640	CE	MET	211	63.095	8.963	26.025
1641	N	THR	212	62.472	12.025	22.370
1642	CA	THR	212	62.704	11.973	20.917
1643	C	THR	212	61.428	11.990	20.078
1644	O	THR	212	60.654	11.022	20.036
1645	CB	THR	212	63.516	10.724	20.582
1646	OG1	THR	212	62.793	9.578	21.008
1647	CG2	THR	212	64.862	10.723	21.296
1648	N	ALA	213	61.417	12.955	19.174
1649	CA	ALA	213	60.283	13.143	18.268
1650	C	ALA	213	60.223	12.096	17.160
1651	O	ALA	213	59.122	11.690	16.784
1652	CB	ALA	213	60.405	14.527	17.641
1653	N	ASP	214	61.346	11.453	16.882
1654	CA	ASP	214	61.392	10.442	15.820
1655	C	ASP	214	60.791	9.111	16.267
1656	O	ASP	214	60.036	8.495	15.505
1657	CB	ASP	214	62.851	10.221	15.434
1658	CG	ASP	214	63.484	11.524	14.953
1659	OD1	ASP	214	64.100	12.192	15.774
1660	OD2	ASP	214	63.304	11.851	13.789
1661	N	GLN	215	60.890	8.823	17.556
1662	CA	GLN	215	60.332	7.569	18.062
1663	C	GLN	215	58.864	7.766	18.406
1664	O	GLN	215	58.042	6.877	18.144
1665	CB	GLN	215	61.126	7.135	19.285
1666	CG	GLN	215	62.579	6.874	18.905
1667	CD	GLN	215	63.393	6.499	20.138
1668	OE1	GLN	215	62.988	6.770	21.273
1669	NE2	GLN	215	64.561	5.930	19.896
1670	N	ALA	216	58.519	9.022	18.639
1671	CA	ALA	216	57.124	9.399	18.840
1672	C	ALA	216	56.364	9.429	17.515
1673	O	ALA	216	55.193	9.035	17.482
1674	CB	ALA	216	57.103	10.783	19.475
1675	N	ILE	217	57.084	9.610	16.419
1676	CA	ILE	217	56.467	9.571	15.091
1677	C	ILE	217	56.199	8.148	14.627
1678	O	ILE	217	55.099	7.882	14.127
1679	CB	ILE	217	57.383	10.289	14.106
1680	CG1	ILE	217	57.254	11.793	14.297
1681	CG2	ILE	217	57.084	9.895	12.666
1682	CD1	ILE	217	55.788	12.204	14.249
1683	N	ILE	218	57.014	7.210	15.082
1684	CA	ILE	218	56.752	5.808	14.753
1685	C	ILE	218	55.648	5.250	15.648
1686	O	ILE	218	54.806	4.482	15.170

1687	CB	ILE	218	58.040	5.015	14.932
1688	CG1	ILE	218	59.150	5.614	14.077
1689	CG2	ILE	218	57.828	3.550	14.565
1690	CD1	ILE	218	60.463	4.863	14.268
1691	N	PHE	219	55.467	5.878	16.799
1692	CA	PHE	219	54.383	5.500	17.707
1693	C	PHE	219	53.045	6.102	17.253
1694	O	PHE	219	51.998	5.458	17.396
1695	CB	PHE	219	54.774	6.017	19.086
1696	CG	PHE	219	54.100	5.316	20.258
1697	CD1	PHE	219	53.657	4.006	20.127
1698	CD2	PHE	219	53.951	5.983	21.466
1699	CE1	PHE	219	53.051	3.369	21.201
1700	CE2	PHE	219	53.345	5.346	22.540
1701	CZ	PHE	219	52.894	4.040	22.406
1702	N	VAL	220	53.122	7.177	16.482
1703	CA	VAL	220	51.942	7.783	15.849
1704	C	VAL	220	51.517	7.005	14.602
1705	O	VAL	220	50.322	6.913	14.291
1706	CB	VAL	220	52.323	9.217	15.479
1707	CG1	VAL	220	51.462	9.805	14.369
1708	CG2	VAL	220	52.339	10.123	16.705
1709	N	ARG	221	52.459	6.272	14.037
1710	CA	ARG	221	52.173	5.371	12.922
1711	C	ARG	221	51.741	3.979	13.380
1712	O	ARG	221	51.435	3.133	12.530
1713	CB	ARG	221	53.448	5.218	12.110
1714	CG	ARG	221	53.920	6.543	11.536
1715	CD	ARG	221	55.208	6.352	10.748
1716	NE	ARG	221	55.636	7.604	10.111
1717	CZ	ARG	221	55.365	7.904	8.839
1718	NH1	ARG	221	54.633	7.069	8.098
1719	NH2	ARG	221	55.808	9.047	8.315
1720	N	ALA	222	51.664	3.754	14.683
1721	CA	ALA	222	51.379	2.412	15.198
1722	C	ALA	222	49.900	2.040	15.278
1723	O	ALA	222	49.584	0.854	15.429
1724	CB	ALA	222	52.005	2.283	16.582
1725	N	LYS	223	49.004	3.005	15.150
1726	CA	LYS	223	47.575	2.667	15.191
1727	C	LYS	223	46.885	2.938	13.857
1728	O	LYS	223	45.687	2.667	13.693
1729	CB	LYS	223	46.900	3.472	16.291
1730	CG	LYS	223	47.630	3.317	17.618
1731	CD	LYS	223	46.938	4.095	18.726
1732	CE	LYS	223	47.809	4.139	19.974
1733	NZ	LYS	223	49.073	4.837	19.697
1734	N	ARG	224	47.666	3.431	12.912
1735	CA	ARG	224	47.147	3.846	11.607
1736	C	ARG	224	48.321	4.292	10.752
1737	O	ARG	224	49.103	5.146	11.190
1738	CB	ARG	224	46.204	5.033	11.801
1739	CG	ARG	224	45.387	5.352	10.551
1740	CD	ARG	224	44.553	6.612	10.753
1741	NE	ARG	224	43.516	6.749	9.718
1742	CZ	ARG	224	42.332	7.317	9.960
1743	NH1	ARG	224	42.083	7.852	11.157
1744	NH2	ARG	224	41.408	7.379	9.001
1745	N	PRO	225	48.481	3.675	9.594
1746	CA	PRO	225	49.468	4.142	8.619
1747	C	PRO	225	49.187	5.576	8.169
1748	O	PRO	225	48.168	5.854	7.529
1749	CB	PRO	225	49.373	3.178	7.476
1750	CG	PRO	225	48.264	2.175	7.752
1751	CD	PRO	225	47.681	2.550	9.103

1752	N	ASN	226	50.051	6.484	8.590
1753	CA	ASN	226	49.907	7.893	8.213
1754	C	ASN	226	51.166	8.475	7.572
1755	O	ASN	226	51.836	7.819	6.767
1756	CB	ASN	226	49.475	8.710	9.432
1757	CG	ASN	226	50.246	8.368	10.705
1758	OD1	ASN	226	51.482	8.407	10.751
1759	ND2	ASN	226	49.477	8.208	11.763
1760	N	SER	227	51.397	9.745	7.864
1761	CA	SER	227	52.518	10.508	7.301
1762	C	SER	227	52.726	11.761	8.141
1763	O	SER	227	51.771	12.228	8.774
1764	CB	SER	227	52.179	10.912	5.871
1765	OG	SER	227	51.010	11.718	5.921
1766	N	ILE	228	53.915	12.338	8.076
1767	CA	ILE	228	54.200	13.523	8.888
1768	C	ILE	228	55.332	14.377	8.291
1769	O	ILE	228	56.360	13.864	7.824
1770	CB	ILE	228	54.507	13.008	10.301
1771	CG1	ILE	228	54.609	14.098	11.363
1772	CG2	ILE	228	55.779	12.168	10.300
1773	CD1	ILE	228	56.030	14.622	11.522
1774	N	GLN	229	55.062	15.672	8.204
1775	CA	GLN	229	56.072	16.676	7.810
1776	C	GLN	229	57.048	16.881	8.970
1777	O	GLN	229	56.891	17.816	9.770
1778	CB	GLN	229	55.411	18.023	7.490
1779	CG	GLN	229	54.343	17.983	6.390
1780	CD	GLN	229	52.947	17.774	6.981
1781	OE1	GLN	229	52.486	16.635	7.123
1782	NE2	GLN	229	52.279	18.870	7.287
1783	N	THR	230	58.161	16.171	8.910
1784	CA	THR	230	59.014	16.015	10.092
1785	C	THR	230	59.873	17.229	10.407
1786	O	THR	230	59.963	17.584	11.587
1787	CB	THR	230	59.896	14.792	9.874
1788	OG1	THR	230	59.044	13.696	9.563
1789	CG2	THR	230	60.705	14.438	11.119
1790	N	ARG	231	60.223	18.023	9.408
1791	CA	ARG	231	61.030	19.217	9.700
1792	C	ARG	231	60.161	20.356	10.238
1793	O	ARG	231	60.612	21.111	11.111
1794	CB	ARG	231	61.757	19.675	8.444
1795	CG	ARG	231	62.753	20.779	8.786
1796	CD	ARG	231	63.495	21.289	7.557
1797	NE	ARG	231	64.480	22.312	7.943
1798	CZ	ARG	231	64.289	23.622	7.765
1799	NH1	ARG	231	63.177	24.062	7.171
1800	NH2	ARG	231	65.223	24.491	8.157
1801	N	GLY	232	58.870	20.269	9.954
1802	CA	GLY	232	57.906	21.230	10.483
1803	C	GLY	232	57.764	20.996	11.979
1804	O	GLY	232	58.006	21.913	12.774
1805	N	GLN	233	57.638	19.730	12.346
1806	CA	GLN	233	57.517	19.368	13.759
1807	C	GLN	233	58.840	19.487	14.525
1808	O	GLN	233	58.814	19.807	15.720
1809	CB	GLN	233	57.028	17.933	13.848
1810	CG	GLN	233	56.808	17.533	15.300
1811	CD	GLN	233	56.588	16.036	15.379
1812	OE1	GLN	233	55.971	15.445	14.486
1813	NE2	GLN	233	57.073	15.444	16.456
1814	N	LEU	234	59.965	19.441	13.831
1815	CA	LEU	234	61.251	19.663	14.498
1816	C	LEU	234	61.388	21.116	14.934

1817	O	LEU	234	61.561	21.367	16.133
1818	CB	LEU	234	62.386	19.307	13.549
1819	CG	LEU	234	62.499	17.804	13.337
1820	CD1	LEU	234	63.564	17.482	12.295
1821	CD2	LEU	234	62.791	17.087	14.651
1822	N	LEU	235	61.009	22.030	14.055
1823	CA	LEU	235	61.052	23.462	14.382
1824	C	LEU	235	59.991	23.830	15.420
1825	O	LEU	235	60.292	24.524	16.403
1826	CB	LEU	235	60.771	24.230	13.096
1827	CG	LEU	235	61.899	24.100	12.080
1828	CD1	LEU	235	61.433	24.513	10.689
1829	CD2	LEU	235	63.115	24.912	12.510
1830	N	CYS	236	58.863	23.145	15.321
1831	CA	CYS	236	57.731	23.292	16.241
1832	C	CYS	236	58.148	22.984	17.676
1833	O	CYS	236	58.174	23.884	18.528
1834	CB	CYS	236	56.717	22.245	15.784
1835	SG	CYS	236	54.977	22.428	16.227
1836	N	VAL	237	58.724	21.807	17.856
1837	CA	VAL	237	59.107	21.361	19.193
1838	C	VAL	237	60.335	22.087	19.730
1839	O	VAL	237	60.288	22.536	20.881
1840	CB	VAL	237	59.393	19.866	19.138
1841	CG1	VAL	237	59.988	19.373	20.451
1842	CG2	VAL	237	58.137	19.078	18.788
1843	N	ARG	238	61.260	22.468	18.863
1844	CA	ARG	238	62.478	23.114	19.358
1845	C	ARG	238	62.259	24.558	19.797
1846	O	ARG	238	62.926	24.995	20.743
1847	CB	ARG	238	63.563	23.055	18.291
1848	CG	ARG	238	64.036	21.621	18.081
1849	CD	ARG	238	65.218	21.556	17.123
1850	NE	ARG	238	64.868	22.091	15.798
1851	CZ	ARG	238	65.183	21.462	14.665
1852	NH1	ARG	238	64.849	21.996	13.489
1853	NH2	ARG	238	65.833	20.297	14.707
1854	N	GLU	239	61.224	25.211	19.294
1855	CA	GLU	239	60.937	26.558	19.784
1856	C	GLU	239	59.984	26.516	20.979
1857	O	GLU	239	60.149	27.300	21.923
1858	CB	GLU	239	60.317	27.376	18.658
1859	CG	GLU	239	60.272	28.867	18.988
1860	CD	GLU	239	61.632	29.523	18.734
1861	OE1	GLU	239	62.520	28.794	18.306
1862	OE2	GLU	239	61.628	30.739	18.600
1863	N	PHE	240	59.178	25.470	21.061
1864	CA	PHE	240	58.205	25.384	22.155
1865	C	PHE	240	58.848	24.846	23.432
1866	O	PHE	240	58.475	25.258	24.537
1867	CB	PHE	240	57.067	24.474	21.715
1868	CG	PHE	240	55.720	24.821	22.340
1869	CD1	PHE	240	55.523	26.072	22.912
1870	CD2	PHE	240	54.683	23.898	22.316
1871	CE1	PHE	240	54.294	26.393	23.474
1872	CE2	PHE	240	53.455	24.219	22.878
1873	CZ	PHE	240	53.261	25.466	23.459
1874	N	THR	241	59.968	24.162	23.268
1875	CA	THR	241	60.747	23.709	24.427
1876	C	THR	241	61.567	24.827	25.066
1877	O	THR	241	61.885	24.710	26.253
1878	CB	THR	241	61.685	22.575	24.028
1879	OG1	THR	241	62.454	22.992	22.905
1880	CG2	THR	241	60.919	21.311	23.655
1881	N	GLN	242	61.686	25.969	24.406

1882	CA	GLN	242	62.369	27.114	25.016
1883	C	GLN	242	61.419	27.821	25.981
1884	O	GLN	242	61.806	28.164	27.108
1885	CB	GLN	242	62.748	28.062	23.892
1886	CG	GLN	242	63.592	27.365	22.837
1887	CD	GLN	242	63.619	28.214	21.573
1888	OE1	GLN	242	62.789	29.116	21.400
1889	NE2	GLN	242	64.482	27.833	20.649
1890	N	PHE	243	60.141	27.719	25.648
1891	CA	PHE	243	59.070	28.208	26.515
1892	C	PHE	243	58.905	27.312	27.737
1893	O	PHE	243	58.722	27.804	28.858
1894	CB	PHE	243	57.781	28.203	25.694
1895	CG	PHE	243	56.495	28.262	26.512
1896	CD1	PHE	243	55.812	27.090	26.815
1897	CD2	PHE	243	55.996	29.482	26.939
1898	CE1	PHE	243	54.649	27.137	27.570
1899	CE2	PHE	243	54.830	29.530	27.692
1900	CZ	PHE	243	54.160	28.358	28.013
1901	N	LEU	244	59.192	26.035	27.547
1902	CA	LEU	244	59.078	25.073	28.637
1903	C	LEU	244	60.281	25.136	29.575
1904	O	LEU	244	60.124	24.955	30.788
1905	CB	LEU	244	59.005	23.685	28.010
1906	CG	LEU	244	58.760	22.589	29.040
1907	CD1	LEU	244	57.442	22.817	29.773
1908	CD2	LEU	244	58.772	21.215	28.380
1909	N	THR	245	61.445	25.483	29.052
1910	CA	THR	245	62.631	25.506	29.913
1911	C	THR	245	63.461	26.790	29.845
1912	O	THR	245	64.191	27.044	28.880
1913	CB	THR	245	63.536	24.318	29.576
1914	OG1	THR	245	63.864	24.360	28.194
1915	CG2	THR	245	62.876	22.973	29.859
1916	N	PRO	246	63.363	27.578	30.903
1917	CA	PRO	246	62.130	27.756	31.682
1918	C	PRO	246	61.264	28.938	31.202
1919	O	PRO	246	60.512	29.493	32.015
1920	CB	PRO	246	62.677	28.110	33.029
1921	CG	PRO	246	64.034	28.776	32.803
1922	CD	PRO	246	64.353	28.571	31.325
1923	N	LEU	247	61.440	29.408	29.975
1924	CA	LEU	247	60.953	30.753	29.656
1925	C	LEU	247	59.526	30.783	29.120
1926	O	LEU	247	59.300	30.898	27.907
1927	CB	LEU	247	61.916	31.394	28.667
1928	CG	LEU	247	61.737	32.908	28.636
1929	CD1	LEU	247	61.841	33.491	30.040
1930	CD2	LEU	247	62.756	33.559	27.710
1931	N	ARG	248	58.631	31.077	30.051
1932	CA	ARG	248	57.195	31.190	29.765
1933	C	ARG	248	56.831	32.488	29.030
1934	O	ARG	248	55.842	32.521	28.282
1935	CB	ARG	248	56.460	31.117	31.100
1936	CG	ARG	248	54.948	31.075	30.919
1937	CD	ARG	248	54.231	30.896	32.252
1938	NE	ARG	248	52.782	30.741	32.046
1939	CZ	ARG	248	52.157	29.563	32.113
1940	NH1	ARG	248	52.846	28.454	32.392
1941	NH2	ARG	248	50.839	29.494	31.909
1942	N	ASN	249	57.792	33.399	28.964
1943	CA	ASN	249	57.619	34.659	28.233
1944	C	ASN	249	57.754	34.469	26.719
1945	O	ASN	249	57.318	35.338	25.955
1946	CB	ASN	249	58.682	35.655	28.690

1947	CG	ASN	249	58.612	35.938	30.192
1948	OD1	ASN	249	57.616	35.656	30.868
1949	ND2	ASN	249	59.692	36.509	30.697
1950	N	ILE	250	58.147	33.279	26.287
1951	CA	ILE	250	58.235	33.000	24.855
1952	C	ILE	250	56.867	32.748	24.218
1953	O	ILE	250	56.710	33.081	23.039
1954	CB	ILE	250	59.194	31.832	24.650
1955	CG1	ILE	250	60.592	32.291	25.035
1956	CG2	ILE	250	59.185	31.311	23.217
1957	CD1	ILE	250	61.640	31.230	24.746
1958	N	PHE	251	55.832	32.538	25.020
1959	CA	PHE	251	54.483	32.489	24.441
1960	C	PHE	251	53.999	33.904	24.120
1961	O	PHE	251	53.466	34.132	23.027
1962	CB	PHE	251	53.523	31.842	25.429
1963	CG	PHE	251	52.080	31.775	24.937
1964	CD1	PHE	251	51.804	31.378	23.634
1965	CD2	PHE	251	51.042	32.107	25.796
1966	CE1	PHE	251	50.489	31.326	23.189
1967	CE2	PHE	251	49.727	32.053	25.351
1968	CZ	PHE	251	49.451	31.665	24.047
1969	N	SER	252	54.530	34.859	24.867
1970	CA	SER	252	54.213	36.271	24.657
1971	C	SER	252	55.084	36.888	23.563
1972	O	SER	252	54.852	38.034	23.168
1973	CB	SER	252	54.441	37.012	25.967
1974	OG	SER	252	53.641	36.382	26.959
1975	N	CYS	253	56.055	36.133	23.071
1976	CA	CYS	253	56.824	36.548	21.899
1977	C	CYS	253	56.288	35.853	20.649
1978	O	CYS	253	56.185	36.474	19.580
1979	CB	CYS	253	58.284	36.169	22.119
1980	SG	CYS	253	59.406	36.564	20.759
1981	N	CYS	254	55.744	34.662	20.843
1982	CA	CYS	254	55.149	33.912	19.732
1983	C	CYS	254	53.789	34.471	19.348
1984	O	CYS	254	53.473	34.505	18.157
1985	CB	CYS	254	54.992	32.445	20.119
1986	SG	CYS	254	56.525	31.502	20.282
1987	N	ASP	255	53.104	35.098	20.288
1988	CA	ASP	255	51.852	35.799	19.963
1989	C	ASP	255	52.055	36.943	18.944
1990	O	ASP	255	51.515	36.807	17.836
1991	CB	ASP	255	51.181	36.283	21.250
1992	CG	ASP	255	50.782	35.099	22.129
1993	OD1	ASP	255	50.766	35.269	23.342
1994	OD2	ASP	255	50.430	34.070	21.569
1995	N	PRO	256	52.873	37.966	19.197
1996	CA	PRO	256	53.062	38.993	18.167
1997	C	PRO	256	53.848	38.544	16.929
1998	O	PRO	256	53.637	39.152	15.877
1999	CB	PRO	256	53.771	40.125	18.844
2000	CG	PRO	256	54.195	39.688	20.231
2001	CD	PRO	256	53.635	38.290	20.410
2002	N	LYS	257	54.577	37.436	16.983
2003	CA	LYS	257	55.275	36.925	15.791
2004	C	LYS	257	54.396	35.967	14.970
2005	O	LYS	257	54.698	35.662	13.810
2006	CB	LYS	257	56.554	36.234	16.264
2007	CG	LYS	257	57.405	35.682	15.122
2008	CD	LYS	257	57.794	36.754	14.112
2009	CE	LYS	257	58.627	36.170	12.978
2010	NZ	LYS	257	59.863	35.563	13.498
2011	N	ALA	258	53.275	35.561	15.543

2012	CA	ALA	258	52.279	34.787	14.802
2013	C	ALA	258	51.330	35.735	14.091
2014	O	ALA	258	50.635	35.345	13.143
2015	CB	ALA	258	51.490	33.927	15.782
2016	N	HIS	259	51.351	36.979	14.546
2017	CA	HIS	259	50.622	38.067	13.896
2018	C	HIS	259	49.127	37.750	13.860
2019	O	HIS	259	48.573	37.492	12.783
2020	CB	HIS	259	51.163	38.213	12.478
2021	CG	HIS	259	52.589	38.699	12.265
2022	ND1	HIS	259	53.367	39.406	13.109
2023	CD2	HIS	259	53.330	38.485	11.128
2024	CE1	HIS	259	54.557	39.642	12.519
2025	NE2	HIS	259	54.534	39.070	11.297
2026	N	ALA	260	48.498	37.865	15.022
2027	CA	ALA	260	47.150	37.325	15.256
2028	C	ALA	260	46.071	38.294	15.757
2029	O	ALA	260	45.088	37.825	16.350
2030	CB	ALA	260	47.297	36.212	16.289
2031	N	VAL	261	46.218	39.591	15.536
2032	CA	VAL	261	45.226	40.568	16.034
2033	C	VAL	261	43.856	40.327	15.381
2034	O	VAL	261	43.785	39.611	14.374
2035	CB	VAL	261	45.810	41.973	15.807
2036	CG1	VAL	261	44.925	42.963	15.060
2037	CG2	VAL	261	46.330	42.585	17.101
2038	N	THR	262	42.783	40.756	16.037
2039	CA	THR	262	41.399	40.544	15.539
2040	C	THR	262	41.018	41.377	14.300
2041	O	THR	262	40.131	42.238	14.338
2042	CB	THR	262	40.421	40.849	16.671
2043	OG1	THR	262	40.629	42.189	17.106
2044	CG2	THR	262	40.643	39.920	17.860
2045	N	LEU	263	41.686	41.070	13.201
2046	CA	LEU	263	41.479	41.693	11.893
2047	C	LEU	263	41.537	40.590	10.837
2048	O	LEU	263	41.860	39.450	11.181
2049	CB	LEU	263	42.596	42.716	11.660
2050	CG	LEU	263	42.390	44.000	12.459
2051	CD1	LEU	263	43.542	44.971	12.228
2052	CD2	LEU	263	41.061	44.659	12.100
2053	N	PRO	264	41.177	40.885	9.593
2054	CA	PRO	264	41.320	39.894	8.510
2055	C	PRO	264	42.766	39.614	8.063
2056	O	PRO	264	42.989	38.701	7.260
2057	CB	PRO	264	40.538	40.462	7.367
2058	CG	PRO	264	40.144	41.894	7.686
2059	CD	PRO	264	40.603	42.149	9.111
2060	N	GLN	265	43.730	40.369	8.565
2061	CA	GLN	265	45.139	40.102	8.263
2062	C	GLN	265	45.712	39.077	9.235
2063	O	GLN	265	45.468	39.166	10.443
2064	CB	GLN	265	45.912	41.390	8.482
2065	CG	GLN	265	45.307	42.576	7.752
2066	CD	GLN	265	45.867	43.836	8.395
2067	OE1	GLN	265	45.727	44.023	9.611
2068	NE2	GLN	265	46.496	44.670	7.587
2069	N	TYR	266	46.477	38.133	8.718
2070	CA	TYR	266	47.222	37.226	9.599
2071	C	TYR	266	48.533	36.814	8.941
2072	O	TYR	266	48.561	36.531	7.737
2073	CB	TYR	266	46.375	35.993	9.892
2074	CG	TYR	266	46.846	35.156	11.082
2075	CD1	TYR	266	47.914	34.282	10.957
2076	CD2	TYR	266	46.168	35.250	12.293

2077	CE1	TYR	266	48.339	33.541	12.052
2078	CE2	TYR	266	46.590	34.511	13.386
2079	CZ	TYR	266	47.687	33.669	13.268
2080	OH	TYR	266	48.270	33.153	14.406
2081	N	LEU	267	49.608	36.969	9.700
2082	CA	LEU	267	50.990	36.553	9.351
2083	C	LEU	267	51.687	37.319	8.204
2084	O	LEU	267	52.908	37.200	8.056
2085	CB	LEU	267	50.964	35.051	9.053
2086	CG	LEU	267	52.348	34.405	9.071
2087	CD1	LEU	267	53.051	34.636	10.406
2088	CD2	LEU	267	52.258	32.913	8.766
2089	N	ILE	268	50.980	38.145	7.452
2090	CA	ILE	268	51.649	38.899	6.387
2091	C	ILE	268	52.075	40.255	6.934
2092	O	ILE	268	53.250	40.481	7.243
2093	CB	ILE	268	50.691	39.048	5.206
2094	CG1	ILE	268	50.062	37.704	4.861
2095	CG2	ILE	268	51.408	39.578	3.968
2096	CD1	ILE	268	49.201	37.824	3.609
2097	N	ARG	269	51.102	41.140	7.063
2098	CA	ARG	269	51.312	42.431	7.731
2099	C	ARG	269	50.438	42.463	8.973
2100	O	ARG	269	49.210	42.553	8.849
2101	CB	ARG	269	50.903	43.596	6.825
2102	CG	ARG	269	51.977	44.083	5.846
2103	CD	ARG	269	52.201	43.159	4.652
2104	NE	ARG	269	53.060	43.788	3.638
2105	CZ	ARG	269	53.875	43.097	2.838
2106	NH1	ARG	269	54.042	41.787	3.030
2107	NH2	ARG	269	54.593	43.730	1.908
2108	N	GLN	270	51.044	42.321	10.140
2109	CA	GLN	270	50.231	42.266	11.360
2110	C	GLN	270	50.936	42.706	12.647
2111	O	GLN	270	51.571	43.768	12.687
2112	CB	GLN	270	49.675	40.859	11.489
2113	CG	GLN	270	48.166	40.801	11.297
2114	CD	GLN	270	47.509	41.516	12.461
2115	OE1	GLN	270	47.850	41.228	13.619
2116	NE2	GLN	270	46.723	42.532	12.148
2117	N	ARG	271	50.917	41.825	13.640
2118	CA	ARG	271	51.167	42.164	15.059
2119	C	ARG	271	52.516	42.735	15.486
2120	O	ARG	271	52.563	43.318	16.574
2121	CB	ARG	271	50.955	40.928	15.915
2122	CG	ARG	271	49.598	40.918	16.595
2123	CD	ARG	271	49.564	39.849	17.678
2124	NE	ARG	271	48.287	39.873	18.398
2125	CZ	ARG	271	48.175	39.580	19.693
2126	NH1	ARG	271	49.260	39.246	20.394
2127	NH2	ARG	271	46.982	39.635	20.288
2128	N	HIS	272	53.533	42.761	14.646
2129	CA	HIS	272	54.746	43.465	15.066
2130	C	HIS	272	54.623	44.982	14.917
2131	O	HIS	272	55.416	45.721	15.510
2132	CB	HIS	272	55.959	42.920	14.330
2133	CG	HIS	272	56.550	41.738	15.067
2134	ND1	HIS	272	56.411	41.487	16.382
2135	CD2	HIS	272	57.324	40.730	14.546
2136	CE1	HIS	272	57.072	40.357	16.696
2137	NE2	HIS	272	57.637	39.890	15.560
2138	N	LEU	273	53.587	45.441	14.231
2139	CA	LEU	273	53.265	46.868	14.245
2140	C	LEU	273	51.779	47.090	14.549
2141	O	LEU	273	51.421	48.002	15.308

2142	CB	LEU	273	53.683	47.545	12.929
2143	CG	LEU	273	53.058	46.979	11.648
2144	CD1	LEU	273	52.735	48.096	10.663
2145	CD2	LEU	273	53.917	45.906	10.976
2146	N	LEU	274	50.958	46.128	14.161
2147	CA	LEU	274	49.504	46.278	14.283
2148	C	LEU	274	48.935	45.785	15.611
2149	O	LEU	274	47.770	46.074	15.906
2150	CB	LEU	274	48.821	45.575	13.117
2151	CG	LEU	274	49.232	46.196	11.783
2152	CD1	LEU	274	48.627	45.438	10.611
2153	CD2	LEU	274	48.849	47.669	11.706
2154	N	HIS	275	49.765	45.207	16.465
2155	CA	HIS	275	49.303	44.912	17.822
2156	C	HIS	275	49.352	46.205	18.621
2157	O	HIS	275	48.359	46.573	19.263
2158	CB	HIS	275	50.224	43.879	18.454
2159	CG	HIS	275	49.801	43.393	19.823
2160	ND1	HIS	275	48.552	43.380	20.328
2161	CD2	HIS	275	50.630	42.878	20.790
2162	CE1	HIS	275	48.583	42.871	21.576
2163	NE2	HIS	275	49.868	42.560	21.861
2164	N	GLY	276	50.365	47.002	18.312
2165	CA	GLY	276	50.497	48.347	18.873
2166	C	GLY	276	49.388	49.236	18.328
2167	O	GLY	276	48.648	49.843	19.109
2168	N	TYR	277	49.162	49.149	17.027
2169	CA	TYR	277	48.084	49.907	16.380
2170	C	TYR	277	46.689	49.582	16.920
2171	O	TYR	277	45.977	50.518	17.301
2172	CB	TYR	277	48.142	49.604	14.889
2173	CG	TYR	277	46.984	50.167	14.072
2174	CD1	TYR	277	46.087	49.298	13.462
2175	CD2	TYR	277	46.831	51.540	13.928
2176	CE1	TYR	277	45.029	49.801	12.718
2177	CE2	TYR	277	45.773	52.045	13.185
2178	CZ	TYR	277	44.874	51.174	12.584
2179	OH	TYR	277	43.804	51.675	11.875
2180	N	GLU	278	46.390	48.317	17.176
2181	CA	GLU	278	45.062	47.975	17.700
2182	C	GLU	278	44.933	48.316	19.184
2183	O	GLU	278	43.861	48.770	19.609
2184	CB	GLU	278	44.793	46.490	17.475
2185	CG	GLU	278	43.383	46.111	17.924
2186	CD	GLU	278	43.087	44.647	17.608
2187	OE1	GLU	278	43.545	43.794	18.358
2188	OE2	GLU	278	42.500	44.392	16.568
2189	N	ALA	279	46.056	48.371	19.882
2190	CA	ALA	279	46.037	48.798	21.278
2191	C	ALA	279	45.847	50.308	21.379
2192	O	ALA	279	45.014	50.743	22.179
2193	CB	ALA	279	47.351	48.398	21.939
2194	N	ARG	280	46.353	51.048	20.403
2195	CA	ARG	280	46.166	52.503	20.384
2196	C	ARG	280	44.787	52.895	19.860
2197	O	ARG	280	44.251	53.932	20.276
2198	CB	ARG	280	47.246	53.137	19.517
2199	CG	ARG	280	48.632	52.850	20.080
2200	CD	ARG	280	49.720	53.554	19.278
2201	NE	ARG	280	49.675	53.180	17.854
2202	CZ	ARG	280	50.687	52.578	17.225
2203	NH1	ARG	280	50.643	52.407	15.902
2204	NH2	ARG	280	51.790	52.248	17.901
2205	N	LEU	281	44.144	51.986	19.142
2206	CA	LEU	281	42.743	52.185	18.772

2207	C	LEU	281	41.882	52.076	20.018
2208	O	LEU	281	41.204	53.048	20.377
2209	CB	LEU	281	42.304	51.115	17.778
2210	CG	LEU	281	43.038	51.213	16.447
2211	CD1	LEU	281	42.662	50.045	15.543
2212	CD2	LEU	281	42.758	52.542	15.753
2213	N	LEU	282	42.214	51.094	20.840
2214	CA	LEU	282	41.483	50.872	22.092
2215	C	LEU	282	41.787	51.938	23.146
2216	O	LEU	282	40.890	52.265	23.927
2217	CB	LEU	282	41.852	49.501	22.662
2218	CG	LEU	282	40.897	48.370	22.263
2219	CD1	LEU	282	40.911	48.056	20.768
2220	CD2	LEU	282	41.220	47.105	23.049
2221	N	LYS	283	42.911	52.629	23.012
2222	CA	LYS	283	43.269	53.704	23.946
2223	C	LYS	283	42.569	55.030	23.661
2224	O	LYS	283	42.520	55.878	24.558
2225	CB	LYS	283	44.771	53.941	23.872
2226	CG	LYS	283	45.564	52.746	24.386
2227	CD	LYS	283	47.047	52.907	24.074
2228	CE	LYS	283	47.829	51.648	24.428
2229	NZ	LYS	283	49.233	51.770	24.004
2230	N	HIS	284	42.012	55.217	22.474
2231	CA	HIS	284	41.229	56.438	22.258
2232	C	HIS	284	39.739	56.119	22.218
2233	O	HIS	284	38.894	57.020	22.284
2234	CB	HIS	284	41.686	57.187	21.006
2235	CG	HIS	284	41.436	56.528	19.665
2236	ND1	HIS	284	42.300	55.763	18.972
2237	CD2	HIS	284	40.290	56.618	18.910
2238	CE1	HIS	284	41.725	55.372	17.820
2239	NE2	HIS	284	40.480	55.897	17.783
2240	N	VAL	285	39.429	54.835	22.162
2241	CA	VAL	285	38.036	54.374	22.231
2242	C	VAL	285	37.418	53.980	23.610
2243	O	VAL	285	36.182	54.045	23.637
2244	CB	VAL	285	37.992	53.180	21.268
2245	CG1	VAL	285	36.726	52.339	21.341
2246	CG2	VAL	285	38.228	53.643	19.835
2247	N	PRO	286	38.098	53.921	24.763
2248	CA	PRO	286	37.892	52.728	25.613
2249	C	PRO	286	36.593	52.685	26.424
2250	O	PRO	286	36.247	51.622	26.949
2251	CB	PRO	286	39.046	52.699	26.566
2252	CG	PRO	286	39.856	53.967	26.421
2253	CD	PRO	286	39.264	54.692	25.236
2254	N	LYS	287	35.870	53.789	26.517
2255	CA	LYS	287	34.638	53.804	27.311
2256	C	LYS	287	33.451	54.400	26.558
2257	O	LYS	287	32.380	54.572	27.153
2258	CB	LYS	287	34.877	54.600	28.592
2259	CG	LYS	287	35.950	53.958	29.470
2260	CD	LYS	287	36.161	54.682	30.801
2261	CE	LYS	287	35.295	54.139	31.941
2262	NZ	LYS	287	33.860	54.429	31.781
2263	N	ILE	288	33.621	54.727	25.288
2264	CA	ILE	288	32.524	55.399	24.587
2265	C	ILE	288	31.492	54.407	24.035
2266	O	ILE	288	31.795	53.520	23.226
2267	CB	ILE	288	33.098	56.320	23.503
2268	CG1	ILE	288	32.021	57.241	22.938
2269	CG2	ILE	288	33.775	55.554	22.373
2270	CD1	ILE	288	31.480	58.179	24.012
2271	N	ILE	289	30.256	54.614	24.464

2272	CA	ILE	289	29.096	53.831	24.008
2273	C	ILE	289	29.032	53.791	22.474
2274	O	ILE	289	29.660	54.619	21.800
2275	CB	ILE	289	27.852	54.489	24.622
2276	CG1	ILE	289	26.565	53.695	24.399
2277	CG2	ILE	289	27.691	55.918	24.114
2278	CD1	ILE	289	25.353	54.411	24.985
2279	N	HIS	290	28.505	52.681	21.969
2280	CA	HIS	290	28.391	52.354	20.529
2281	C	HIS	290	29.670	51.717	19.987
2282	O	HIS	290	29.666	50.518	19.683
2283	CB	HIS	290	28.015	53.567	19.675
2284	CG	HIS	290	26.680	54.193	20.023
2285	ND1	HIS	290	25.463	53.686	19.753
2286	CD2	HIS	290	26.481	55.391	20.668
2287	CE1	HIS	290	24.517	54.525	20.221
2288	NE2	HIS	290	25.148	55.579	20.787
2289	N	LEU	291	30.789	52.412	20.100
2290	CA	LEU	291	32.033	51.859	19.564
2291	C	LEU	291	32.629	50.847	20.540
2292	O	LEU	291	32.973	49.733	20.124
2293	CB	LEU	291	33.004	52.998	19.285
2294	CG	LEU	291	34.173	52.519	18.433
2295	CD1	LEU	291	33.679	51.767	17.201
2296	CD2	LEU	291	35.061	53.689	18.029
2297	N	VAL	292	32.408	51.086	21.822
2298	CA	VAL	292	32.774	50.101	22.846
2299	C	VAL	292	31.684	49.050	23.046
2300	O	VAL	292	31.981	47.952	23.527
2301	CB	VAL	292	33.104	50.844	24.135
2302	CG1	VAL	292	33.169	49.957	25.371
2303	CG2	VAL	292	34.420	51.570	23.949
2304	N	CYS	293	30.541	49.248	22.411
2305	CA	CYS	293	29.507	48.217	22.453
2306	C	CYS	293	29.878	47.126	21.455
2307	O	CYS	293	29.913	45.945	21.823
2308	CB	CYS	293	28.164	48.833	22.084
2309	SG	CYS	293	26.763	47.692	22.050
2310	N	LYS	294	30.471	47.555	20.351
2311	CA	LYS	294	30.979	46.614	19.352
2312	C	LYS	294	32.304	46.015	19.810
2313	O	LYS	294	32.482	44.793	19.728
2314	CB	LYS	294	31.204	47.384	18.059
2315	CG	LYS	294	29.934	48.104	17.628
2316	CD	LYS	294	30.194	49.019	16.440
2317	CE	LYS	294	28.946	49.812	16.072
2318	NZ	LYS	294	29.217	50.721	14.947
2319	N	LEU	295	33.079	46.808	20.531
2320	CA	LEU	295	34.361	46.341	21.066
2321	C	LEU	295	34.179	45.257	22.127
2322	O	LEU	295	34.752	44.171	21.973
2323	CB	LEU	295	35.077	47.537	21.681
2324	CG	LEU	295	36.442	47.161	22.244
2325	CD1	LEU	295	37.346	46.611	21.146
2326	CD2	LEU	295	37.089	48.363	22.923
2327	N	LEU	296	33.212	45.429	23.014
2328	CA	LEU	296	32.970	44.417	24.046
2329	C	LEU	296	32.164	43.239	23.519
2330	O	LEU	296	32.369	42.116	23.992
2331	CB	LEU	296	32.243	45.050	25.223
2332	CG	LEU	296	33.133	46.049	25.951
2333	CD1	LEU	296	32.373	46.714	27.092
2334	CD2	LEU	296	34.400	45.377	26.471
2335	N	LEU	297	31.474	43.427	22.406
2336	CA	LEU	297	30.824	42.294	21.751

2337	C	LEU	297	31.868	41.426	21.055
2338	O	LEU	297	31.866	40.206	21.252
2339	CB	LEU	297	29.826	42.822	20.728
2340	CG	LEU	297	29.079	41.686	20.039
2341	CD1	LEU	297	28.331	40.828	21.055
2342	CD2	LEU	297	28.121	42.228	18.986
2343	N	ASP	298	32.913	42.063	20.547
2344	CA	ASP	298	34.019	41.333	19.921
2345	C	ASP	298	34.895	40.655	20.971
2346	O	ASP	298	35.296	39.505	20.767
2347	CB	ASP	298	34.881	42.314	19.129
2348	CG	ASP	298	34.088	42.994	18.016
2349	OD1	ASP	298	33.227	42.337	17.444
2350	OD2	ASP	298	34.453	44.109	17.664
2351	N	LEU	299	34.934	41.230	22.164
2352	CA	LEU	299	35.699	40.648	23.277
2353	C	LEU	299	34.935	39.529	23.991
2354	O	LEU	299	35.540	38.725	24.710
2355	CB	LEU	299	36.024	41.752	24.284
2356	CG	LEU	299	37.442	42.316	24.157
2357	CD1	LEU	299	37.735	42.931	22.791
2358	CD2	LEU	299	37.703	43.343	25.252
2359	N	ALA	300	33.634	39.452	23.757
2360	CA	ALA	300	32.828	38.332	24.252
2361	C	ALA	300	32.707	37.241	23.190
2362	O	ALA	300	32.213	36.139	23.458
2363	CB	ALA	300	31.442	38.849	24.619
2364	N	GLU	301	33.155	37.558	21.989
2365	CA	GLU	301	33.195	36.566	20.927
2366	C	GLU	301	34.561	35.897	20.900
2367	O	GLU	301	34.582	34.684	21.068
2368	CB	GLU	301	32.883	37.222	19.587
2369	CG	GLU	301	31.460	37.771	19.529
2370	CD	GLU	301	30.432	36.681	19.818
2371	OE1	GLU	301	29.425	37.000	20.433
2372	OE2	GLU	301	30.688	35.542	19.449
2373	OXT	GLU	301	35.530	36.567	20.587

Table IX

Atom No	Atom name	Residue	Residue No	x coord	y coord	z coord
1	N	MET	1	1.491	5.335	9.487
5	CA	MET	1	2.465	4.265	9.217
6	CB	MET	1	2.302	3.734	7.795
7	CG	MET	1	0.916	3.146	7.555
8	SD	MET	1	0.637	2.487	5.894
9	CE	MET	1	-1.071	1.927	6.088
10	C	MET	1	3.899	4.759	9.385
11	O	MET	1	4.181	5.962	9.368
12	N	GLY	2	4.795	3.807	9.565
14	CA	GLY	2	6.223	4.121	9.650
15	C	GLY	2	6.848	3.946	8.275
16	O	GLY	2	7.036	2.817	7.808
17	N	VAL	3	7.195	5.058	7.649
19	CA	VAL	3	7.712	4.996	6.279
20	CB	VAL	3	7.307	6.264	5.538
21	CG1	VAL	3	5.795	6.314	5.406
22	CG2	VAL	3	7.819	7.525	6.223
23	C	VAL	3	9.223	4.793	6.234
24	O	VAL	3	9.760	4.480	5.165
25	N	GLN	4	9.859	5.000	7.381
27	CA	GLN	4	11.277	4.693	7.677
28	CB	GLN	4	12.266	5.066	6.568
29	CG	GLN	4	12.590	3.899	5.628
30	CD	GLN	4	13.264	2.728	6.347
31	OE1	GLN	4	12.720	2.136	7.287
32	NE2	GLN	4	14.429	2.364	5.841
35	C	GLN	4	11.684	5.427	8.942
36	O	GLN	4	12.123	6.584	8.860
37	N	PRO	5	11.671	4.714	10.060
38	CA	PRO	5	11.800	5.329	11.392
39	CB	PRO	5	11.830	4.177	12.351
40	CG	PRO	5	11.564	2.883	11.597
41	CD	PRO	5	11.397	3.276	10.139
42	C	PRO	5	13.051	6.203	11.511
43	O	PRO	5	14.083	5.883	10.911
44	N	PRO	6	12.944	7.340	12.189
45	CA	PRO	6	11.729	7.784	12.906
46	CB	PRO	6	12.248	8.754	13.921
47	CG	PRO	6	13.660	9.172	13.541
48	CD	PRO	6	14.056	8.277	12.379
49	C	PRO	6	10.660	8.489	12.051
50	O	PRO	6	9.716	9.063	12.611
51	N	ASN	7	10.857	8.539	10.745
53	CA	ASN	7	9.926	9.200	9.833
54	CB	ASN	7	10.606	9.316	8.470
55	CG	ASN	7	11.924	10.089	8.588
56	OD1	ASN	7	11.916	11.300	8.837
57	ND2	ASN	7	13.033	9.386	8.417
60	C	ASN	7	8.597	8.456	9.689
61	O	ASN	7	8.533	7.261	9.358
62	N	PHE	8	7.553	9.199	10.020
64	CA	PHE	8	6.150	8.809	9.821
65	CB	PHE	8	5.392	8.898	11.140
66	CG	PHE	8	5.888	7.982	12.252
67	CD1	PHE	8	5.687	6.612	12.162

68	CE1	PHE	8	6.130	5.775	13.177
69	CZ	PHE	8	6.771	6.309	14.287
70	CE2	PHE	8	6.966	7.681	14.379
71	CD2	PHE	8	6.524	8.518	13.364
72	C	PHE	8	5.507	9.783	8.837
73	O	PHE	8	4.278	9.890	8.725
74	N	SER	9	6.363	10.593	8.240
76	CA	SER	9	5.939	11.629	7.296
77	CB	SER	9	7.187	12.341	6.785
78	OG	SER	9	7.860	12.896	7.909
79	C	SER	9	5.149	11.062	6.120
80	O	SER	9	5.273	9.875	5.797
81	N	TRP	10	4.124	11.825	5.769
83	CA	TRP	10	3.278	11.625	4.582
84	CB	TRP	10	4.120	11.113	3.417
85	CG	TRP	10	3.363	10.272	2.411
86	CD1	TRP	10	2.272	10.620	1.641
87	NE1	TRP	10	1.907	9.534	0.913
89	CE2	TRP	10	2.716	8.486	1.157
90	CZ2	TRP	10	2.726	7.175	0.704
91	CH2	TRP	10	3.703	6.302	1.162
92	CZ3	TRP	10	4.671	6.721	2.063
93	CE3	TRP	10	4.662	8.032	2.533
94	CD2	TRP	10	3.682	8.905	2.087
95	C	TRP	10	2.055	10.739	4.804
96	O	TRP	10	0.959	11.140	4.401
97	N	VAL	11	2.199	9.670	5.571
99	CA	VAL	11	1.107	8.704	5.726
100	CB	VAL	11	1.720	7.350	6.036
101	CG1	VAL	11	2.189	6.629	4.780
102	CG2	VAL	11	2.857	7.524	7.030
103	C	VAL	11	0.112	9.064	6.822
104	O	VAL	11	−0.896	8.367	6.979
105	N	LEU	12	0.369	10.124	7.569
107	CA	LEU	12	−0.601	10.515	8.591
108	CB	LEU	12	0.091	11.328	9.674
109	CG	LEU	12	1.079	10.478	10.462
110	CD1	LEU	12	1.786	11.316	11.520
111	CD2	LEU	12	0.378	9.287	11.108
112	C	LEU	12	−1.777	11.285	7.989
113	O	LEU	12	−1.621	12.283	7.269
114	N	PRO	13	−2.957	10.743	8.241
115	CA	PRO	13	−4.199	11.444	7.950
116	CB	PRO	13	−5.273	10.409	8.098
117	CG	PRO	13	−4.680	9.188	8.784
118	CD	PRO	13	−3.195	9.477	8.939
119	C	PRO	13	−4.408	12.575	8.944
120	O	PRO	13	−3.895	12.543	10.069
121	N	GLY	14	−5.316	13.464	8.588
123	CA	GLY	14	−5.657	14.607	9.443
124	C	GLY	14	−6.418	14.212	10.707
125	O	GLY	14	−6.397	14.939	11.706
126	N	ARG	15	−7.001	13.023	10.689
128	CA	ARG	15	−7.730	12.499	11.846
129	CB	ARG	15	−8.661	11.403	11.348
130	CG	ARG	15	−9.606	11.903	10.265
131	CD	ARG	15	−10.433	10.749	9.714
132	NE	ARG	15	−9.549	9.689	9.203
133	CZ	ARG	15	−9.713	8.395	9.487
134	NH1	ARG	15	−8.852	7.493	9.009

135	NH2	ARG	15	−10.724	8.004	10.266
136	C	ARG	15	−6.826	11.893	12.923
137	O	ARG	15	−7.320	11.614	14.022
138	N	LEU	16	−5.536	11.752	12.655
140	CA	LEU	16	−4.617	11.203	13.658
141	CB	LEU	16	−4.132	9.836	13.175
142	CG	LEU	16	−3.840	8.860	14.315
143	CD1	LEU	16	−2.597	9.224	15.121
144	CD2	LEU	16	−5.051	8.686	15.225
145	C	LEU	16	−3.444	12.172	13.827
146	O	LEU	16	−2.326	11.909	13.361
147	N	ALA	17	−3.711	13.270	14.517
149	CA	ALA	17	−2.708	14.334	14.650
150	CB	ALA	17	−2.682	15.115	13.345
151	C	ALA	17	−2.995	15.299	15.798
152	O	ALA	17	−4.154	15.507	16.176
153	N	GLY	18	−1.933	15.892	16.324
155	CA	GLY	18	−2.057	16.952	17.334
156	C	GLY	18	−1.412	16.613	18.680
157	O	GLY	18	−1.545	17.402	19.618
158	N	LEU	19	−0.564	15.591	18.666
160	CA	LEU	19	0.035	14.921	19.847
161	CB	LEU	19	1.544	14.920	19.643
162	CG	LEU	19	2.278	13.938	20.552
163	CD1	LEU	19	3.524	13.459	19.855
164	CD2	LEU	19	2.635	14.450	21.947
165	C	LEU	19	−0.256	15.506	21.230
166	O	LEU	19	0.213	16.608	21.556
167	N	ALA	20	−0.944	14.702	22.032
169	CA	ALA	20	−1.162	14.939	23.474
170	CB	ALA	20	−1.564	16.392	23.784
171	C	ALA	20	−2.231	14.008	24.032
172	O	ALA	20	−2.310	12.826	23.693
173	N	LEU	21	−3.100	14.615	24.826
175	CA	LEU	21	−4.236	13.948	25.491
176	CB	LEU	21	−4.835	14.975	26.447
177	CG	LEU	21	−3.851	15.345	27.552
178	CD1	LEU	21	−4.420	16.451	28.432
179	CD2	LEU	21	−3.485	14.119	28.391
180	C	LEU	21	−5.294	13.449	24.494
181	O	LEU	21	−5.094	13.581	23.281
182	N	PRO	22	−6.300	12.717	24.959
183	CA	PRO	22	−7.377	12.247	24.063
184	CB	PRO	22	−7.896	11.023	24.748
185	CG	PRO	22	−7.465	11.055	26.210
186	CD	PRO	22	−6.505	12.227	26.331
187	C	PRO	22	−8.553	13.223	23.820
188	O	PRO	22	−9.529	12.809	23.185
189	N	ARG	23	−8.486	14.464	24.285
191	CA	ARG	23	−9.667	15.352	24.237
192	CB	ARG	23	−10.046	15.734	25.662
193	CG	ARG	23	−10.456	14.530	26.501
194	CD	ARG	23	−10.859	14.964	27.907
195	NE	ARG	23	−11.985	15.913	27.853
196	CZ	ARG	23	−12.838	16.111	28.862
197	NH1	ARG	23	−12.714	15.413	29.993
198	NH2	ARG	23	−13.836	16.986	28.726
199	C	ARG	23	−9.450	16.656	23.456
200	O	ARG	23	−9.149	17.686	24.069
201	N	LEU	24	−9.665	16.608	22.147

203	CA	LEU	24	-9.565	17.774	21.233
204	CB	LEU	24	-8.127	18.307	21.278
205	CG	LEU	24	-8.022	19.818	21.495
206	CD1	LEU	24	-9.006	20.340	22.532
207	CD2	LEU	24	-6.596	20.227	21.837
208	C	LEU	24	-10.003	17.234	19.852
209	O	LEU	24	-10.485	16.097	19.870
210	N	PRO	25	-9.995	17.987	18.748
211	CA	PRO	25	-10.621	17.497	17.498
212	CB	PRO	25	-10.371	18.560	16.469
213	CG	PRO	25	-9.727	19.760	17.133
214	CD	PRO	25	-9.583	19.392	18.599
215	C	PRO	25	-10.094	16.145	17.008
216	O	PRO	25	-10.704	15.105	17.284
217	N	ALA	26	-8.992	16.170	16.273
219	CA	ALA	26	-8.388	14.935	15.754
220	CB	ALA	26	-7.240	15.296	14.821
221	C	ALA	26	-7.869	14.076	16.898
222	O	ALA	26	-7.708	14.561	18.027
223	N	HIS	27	-7.646	12.801	16.628
225	CA	HIS	27	-7.168	11.940	17.701
226	CB	HIS	27	-7.678	10.528	17.541
227	CG	HIS	27	-7.659	9.815	18.875
228	ND1	HIS	27	-7.725	8.493	19.089
230	CE1	HIS	27	-7.678	8.251	20.413
231	NE2	HIS	27	-7.587	9.443	21.046
232	CD2	HIS	27	-7.580	10.418	20.109
233	C	HIS	27	-5.650	11.995	17.761
234	O	HIS	27	-4.904	11.498	16.911
235	N	TYR	28	-5.217	12.620	18.834
237	CA	TYR	28	-3.826	12.997	19.016
238	CB	TYR	28	-3.804	14.505	19.215
239	CG	TYR	28	-4.532	15.170	20.393
240	CD1	TYR	28	-3.833	16.119	21.131
241	CE1	TYR	28	-4.425	16.747	22.214
242	CZ	TYR	28	-5.740	16.451	22.543
243	OH	TYR	28	-6.264	16.927	23.728
244	CE2	TYR	28	-6.466	15.559	21.768
245	CD2	TYR	28	-5.868	14.931	20.690
246	C	TYR	28	-3.110	12.230	20.131
247	O	TYR	28	-1.874	12.301	20.225
248	N	GLN	29	-3.839	11.342	20.788
250	CA	GLN	29	-3.247	10.517	21.843
251	CB	GLN	29	-4.385	9.917	22.672
252	CG	GLN	29	-3.869	9.030	23.803
253	CD	GLN	29	-3.143	9.854	24.860
254	OE1	GLN	29	-3.757	10.673	25.555
255	NE2	GLN	29	-1.871	9.544	25.050
258	C	GLN	29	-2.375	9.394	21.285
259	O	GLN	29	-1.329	9.088	21.874
260	N	PHE	30	-2.619	9.006	20.041
262	CA	PHE	30	-1.791	7.952	19.436
263	CB	PHE	30	-2.497	7.342	18.237
264	CG	PHE	30	-3.503	6.261	18.605
265	CD1	PHE	30	-3.079	5.135	19.297
266	CE1	PHE	30	-3.990	4.144	19.638
267	CZ	PHE	30	-5.326	4.279	19.282
268	CE2	PHE	30	-5.749	5.403	18.584
269	CD2	PHE	30	-4.837	6.395	18.244
270	C	PHE	30	-0.414	8.447	19.020

271	O	PHE	30	0.547	7.686	19.186
272	N	LEU	31	−0.264	9.749	18.837
274	CA	LEU	31	1.061	10.274	18.516
275	CB	LEU	31	0.934	11.609	17.795
276	CG	LEU	31	0.348	11.458	16.398
277	CD1	LEU	31	0.303	12.815	15.710
278	CD2	LEU	31	1.167	10.478	15.563
279	C	LEU	31	1.892	10.448	19.782
280	O	LEU	31	3.110	10.218	19.744
281	N	LEU	32	1.213	10.543	20.917
283	CA	LEU	32	1.912	10.610	22.202
284	CB	LEU	32	0.954	11.175	23.258
285	CG	LEU	32	1.612	11.511	24.603
286	CD1	LEU	32	0.816	12.572	25.350
287	CD2	LEU	32	1.833	10.299	25.506
288	C	LEU	32	2.376	9.206	22.566
289	O	LEU	32	3.512	9.037	23.018
290	N	ASP	33	1.651	8.222	22.058
292	CA	ASP	33	2.010	6.818	22.275
293	CB	ASP	33	0.774	5.950	22.040
294	CG	ASP	33	−0.431	6.392	22.875
295	OD1	ASP	33	−0.238	6.939	23.956
296	OD2	ASP	33	−1.543	6.171	22.412
297	C	ASP	33	3.118	6.362	21.315
298	O	ASP	33	3.711	5.298	21.525
299	N	LEU	34	3.419	7.166	20.305
301	CA	LEU	34	4.511	6.851	19.378
302	CB	LEU	34	4.052	7.158	17.956
303	CG	LEU	34	2.922	6.235	17.514
304	CD1	LEU	34	2.354	6.672	16.169
305	CD2	LEU	34	3.385	4.782	17.460
306	C	LEU	34	5.785	7.647	19.675
307	O	LEU	34	6.847	7.328	19.125
308	N	GLY	35	5.682	8.668	20.512
310	CA	GLY	35	6.859	9.465	20.889
311	C	GLY	35	7.265	10.450	19.793
312	O	GLY	35	8.458	10.628	19.505
313	N	VAL	36	6.268	11.034	19.151
315	CA	VAL	36	6.521	12.009	18.082
316	CB	VAL	36	5.254	12.078	17.224
317	CG1	VAL	36	5.331	13.109	16.106
318	CG2	VAL	36	4.917	10.708	16.646
319	C	VAL	36	6.891	13.362	18.699
320	O	VAL	36	6.422	13.691	19.792
321	N	ARG	37	7.864	14.042	18.120
323	CA	ARG	37	8.238	15.361	18.639
324	CB	ARG	37	9.693	15.329	19.087
325	CG	ARG	37	9.893	14.311	20.204
326	CD	ARG	37	9.104	14.678	21.455
327	NE	ARG	37	9.179	13.596	22.448
328	CZ	ARG	37	8.463	13.591	23.575
329	NH1	ARG	37	7.657	14.618	23.857
330	NH2	ARG	37	8.571	12.571	24.429
331	C	ARG	37	8.034	16.436	17.584
332	O	ARG	37	7.786	17.608	17.905
333	N	HIS	38	8.139	16.027	16.332
335	CA	HIS	38	7.888	16.951	15.219
336	CB	HIS	38	9.023	16.869	14.206
337	CG	HIS	38	10.205	17.779	14.482
338	ND1	HIS	38	10.966	17.831	15.593

340	CE1	HIS	38	11.916	18.774	15.440
341	NE2	HIS	38	11.751	19.325	14.216
342	CD2	HIS	38	10.702	18.721	13.615
343	C	HIS	38	6.569	16.626	14.536
344	O	HIS	38	6.286	15.454	14.257
345	N	LEU	39	5.793	17.660	14.264
347	CA	LEU	39	4.482	17.485	13.632
348	CB	LEU	39	3.408	17.536	14.710
349	CG	LEU	39	2.030	17.272	14.114
350	CD1	LEU	39	1.905	15.823	13.654
351	CD2	LEU	39	0.936	17.606	15.114
352	C	LEU	39	4.203	18.580	12.602
353	O	LEU	39	3.881	19.719	12.956
354	N	VAL	40	4.302	18.235	11.332
356	CA	VAL	40	4.016	19.234	10.292
357	CB	VAL	40	5.123	19.172	9.240
358	CG1	VAL	40	4.983	20.265	8.183
359	CG2	VAL	40	6.492	19.273	9.902
360	C	VAL	40	2.627	19.002	9.684
361	O	VAL	40	2.229	17.856	9.445
362	N	SER	41	1.867	20.078	9.562
364	CA	SER	41	0.526	20.034	8.961
365	CB	SER	41	-0.424	20.839	9.847
366	OG	SER	41	-1.720	20.853	9.249
367	C	SER	41	0.551	20.681	7.584
368	O	SER	41	0.581	21.912	7.507
369	N	LEU	42	0.423	19.890	6.530
371	CA	LEU	42	0.473	20.457	5.169
372	CB	LEU	42	1.040	19.439	4.187
373	CG	LEU	42	2.561	19.439	4.205
374	CD1	LEU	42	3.098	18.599	3.056
375	CD2	LEU	42	3.089	20.859	4.070
376	C	LEU	42	-0.865	20.942	4.621
377	O	LEU	42	-0.890	21.612	3.582
378	N	THR	43	-1.949	20.668	5.323
380	CA	THR	43	-3.266	21.116	4.856
381	CB	THR	43	-4.205	19.919	4.924
382	OG1	THR	43	-3.537	18.825	4.317
383	CG2	THR	43	-5.511	20.151	4.171
384	C	THR	43	-3.789	22.276	5.708
385	O	THR	43	-4.857	22.835	5.428
386	N	GLU	44	-2.938	22.735	6.612
388	CA	GLU	44	-3.326	23.674	7.668
389	CB	GLU	44	-3.472	25.086	7.107
390	CG	GLU	44	-3.808	26.101	8.198
391	CD	GLU	44	-2.818	25.947	9.340
392	OE1	GLU	44	-1.659	26.254	9.101
393	OE2	GLU	44	-3.167	25.267	10.304
394	C	GLU	44	-4.610	23.234	8.359
395	O	GLU	44	-5.693	23.788	8.142
396	N	ARG	45	-4.467	22.225	9.195
398	CA	ARG	45	-5.610	21.795	10.000
399	CB	ARG	45	-6.112	20.443	9.512
400	CG	ARG	45	-4.998	19.413	9.440
401	CD	ARG	45	-5.533	18.082	8.933
402	NE	ARG	45	-6.158	18.243	7.613
403	CZ	ARG	45	-7.360	17.748	7.307
404	NH1	ARG	45	-7.936	18.074	6.149
405	NH2	ARG	45	-8.042	17.044	8.214
406	C	ARG	45	-5.271	21.765	11.484

407	O	ARG	45	-5.920	21.050	12.257
408	N	GLY	46	-4.287	22.556	11.883
410	CA	GLY	46	-3.879	22.543	13.291
411	C	GLY	46	-2.936	23.682	13.673
412	O	GLY	46	-1.737	23.644	13.379
413	N	PRO	47	-3.489	24.660	14.373
414	CA	PRO	47	-2.680	25.637	15.110
415	CB	PRO	47	-3.673	26.591	15.703
416	CG	PRO	47	-5.080	26.075	15.456
417	CD	PRO	47	-4.919	24.787	14.669
418	C	PRO	47	-1.843	24.947	16.187
419	O	PRO	47	-2.299	23.969	16.796
420	N	PRO	48	-0.721	25.557	16.550
421	CA	PRO	48	0.272	24.897	17.414
422	CB	PRO	48	1.522	25.708	17.256
423	CG	PRO	48	1.197	26.987	16.502
424	CD	PRO	48	-0.262	26.872	16.096
425	C	PRO	48	-0.127	24.827	18.891
426	O	PRO	48	0.454	24.032	19.638
427	N	HIS	49	-1.260	25.425	19.224
429	CA	HIS	49	-1.739	25.515	20.602
430	CB	HIS	49	-2.794	26.615	20.655
431	CG	HIS	49	-2.372	27.894	19.956
432	ND1	HIS	49	-1.423	28.759	20.362
434	CE1	HIS	49	-1.329	29.769	19.473
435	NE2	HIS	49	-2.234	29.539	18.494
436	CD2	HIS	49	-2.886	28.389	18.780
437	C	HIS	49	-2.352	24.199	21.072
438	O	HIS	49	-2.217	23.859	22.254
439	N	SER	50	-2.702	23.347	20.119
441	CA	SER	50	-3.216	22.015	20.457
442	CB	SER	50	-3.907	21.431	19.225
443	OG	SER	50	-2.950	21.313	18.179
444	C	SER	50	-2.084	21.083	20.903
445	O	SER	50	-2.283	20.257	21.799
446	N	ASP	51	-0.872	21.410	20.479
448	CA	ASP	51	0.321	20.654	20.852
449	CB	ASP	51	1.157	20.376	19.601
450	CG	ASP	51	0.496	19.364	18.665
451	OD1	ASP	51	-0.494	19.737	18.049
452	OD2	ASP	51	1.186	18.410	18.320
453	C	ASP	51	1.168	21.440	21.843
454	O	ASP	51	2.274	21.009	22.193
455	N	SER	52	0.634	22.550	22.336
457	CA	SER	52	1.413	23.466	23.179
458	CB	SER	52	0.802	24.858	23.083
459	OG	SER	52	1.568	25.732	23.898
460	C	SER	52	1.470	23.023	24.641
461	O	SER	52	2.359	23.465	25.382
462	N	CYS	53	0.635	22.067	25.019
464	CA	CYS	53	0.740	21.518	26.376
465	CB	CYS	53	-0.570	20.835	26.765
466	SG	CYS	53	-2.008	21.929	26.788
467	C	CYS	53	1.979	20.611	26.536
468	O	CYS	53	2.767	20.904	27.440
469	N	PRO	54	2.189	19.558	25.743
470	CA	PRO	54	3.504	18.890	25.774
471	CB	PRO	54	3.262	17.546	25.163
472	CG	PRO	54	1.899	17.549	24.486
473	CD	PRO	54	1.299	18.920	24.756

474	C	PRO	54	4.637	19.621	25.023
475	O	PRO	54	5.793	19.194	25.124
476	N	GLY	55	4.325	20.660	24.261
478	CA	GLY	55	5.357	21.460	23.588
479	C	GLY	55	5.925	20.770	22.348
480	O	GLY	55	7.122	20.465	22.285
481	N	LEU	56	5.065	20.510	21.379
483	CA	LEU	56	5.513	19.864	20.131
484	CB	LEU	56	4.428	19.013	19.467
485	CG	LEU	56	4.179	17.665	20.127
486	CD1	LEU	56	5.480	16.994	20.538
487	CD2	LEU	56	3.241	17.785	21.326
488	C	LEU	56	5.967	20.884	19.104
489	O	LEU	56	5.544	22.047	19.114
490	N	THR	57	6.706	20.384	18.131
492	CA	THR	57	7.177	21.224	17.028
493	CB	THR	57	8.523	20.687	16.562
494	OG1	THR	57	9.308	20.384	17.709
495	CG2	THR	57	9.268	21.705	15.708
496	C	THR	57	6.183	21.179	15.871
497	O	THR	57	6.384	20.437	14.901
498	N	LEU	58	5.091	21.913	16.020
500	CA	LEU	58	4.046	21.941	14.992
501	CB	LEU	58	2.690	22.178	15.663
502	CG	LEU	58	1.500	21.585	14.893
503	CD1	LEU	58	0.230	21.637	15.731
504	CD2	LEU	58	1.235	22.237	13.539
505	C	LEU	58	4.343	23.041	13.977
506	O	LEU	58	4.370	24.233	14.307
507	N	HIS	59	4.574	22.631	12.743
509	CA	HIS	59	4.785	23.612	11.675
510	CB	HIS	59	6.137	23.380	11.021
511	CG	HIS	59	7.277	23.803	11.928
512	ND1	HIS	59	7.252	24.797	12.839
514	CE1	HIS	59	8.452	24.877	13.445
515	NE2	HIS	59	9.242	23.914	12.919
516	CD2	HIS	59	8.529	23.240	11.990
517	C	HIS	59	3.630	23.602	10.680
518	O	HIS	59	3.236	22.562	10.138
519	N	ARG	60	3.090	24.790	10.472
521	CA	ARG	60	1.839	24.962	9.727
522	CB	ARG	60	1.040	26.008	10.485
523	CG	ARG	60	0.871	25.621	11.944
524	CD	ARG	60	0.279	26.776	12.733
525	NE	ARG	60	−1.075	27.109	12.272
526	CZ	ARG	60	−1.714	28.225	12.627
527	NH1	ARG	60	−1.103	29.125	13.399
528	NH2	ARG	60	−2.954	28.452	12.192
529	C	ARG	60	2.037	25.465	8.301
530	O	ARG	60	2.521	26.582	8.083
531	N	LEU	61	1.661	24.633	7.346
533	CA	LEU	61	1.677	25.024	5.929
534	CB	LEU	61	2.781	24.264	5.195
535	CG	LEU	61	4.172	24.567	5.751
536	CD1	LEU	61	5.239	23.709	5.080
537	CD2	LEU	61	4.515	26.046	5.613
538	C	LEU	61	0.320	24.711	5.300
539	O	LEU	61	−0.362	23.771	5.721
540	N	ARG	62	−0.099	25.514	4.340
542	CA	ARG	62	−1.389	25.242	3.696

543	CB	ARG	62	-2.382	26.360	3.979
544	CG	ARG	62	-3.774	25.940	3.515
545	CD	ARG	62	-4.804	27.039	3.737
546	NE	ARG	62	-4.488	28.219	2.920
547	CZ	ARG	62	-5.233	28.603	1.881
548	NH1	ARG	62	-4.894	29.690	1.184
549	NH2	ARG	62	-6.320	27.905	1.543
550	C	ARG	62	-1.234	25.083	2.193
551	O	ARG	62	-1.238	26.060	1.435
552	N	ILE	63	-1.078	23.840	1.781
554	CA	ILE	63	-0.983	23.526	0.360
555	CB	ILE	63	0.271	22.682	0.139
556	CG2	ILE	63	0.477	22.375	-1.341
557	CG1	ILE	63	1.497	23.395	0.698
558	CD1	ILE	63	2.764	22.580	0.472
559	C	ILE	63	-2.228	22.761	-0.077
560	O	ILE	63	-2.542	21.699	0.468
561	N	PRO	64	-2.985	23.354	-0.984
562	CA	PRO	64	-4.024	22.601	-1.685
563	CB	PRO	64	-4.708	23.605	-2.561
564	CG	PRO	64	-3.951	24.926	-2.494
565	CD	PRO	64	-2.806	24.706	-1.518
566	C	PRO	64	-3.379	21.493	-2.507
567	O	PRO	64	-2.364	21.730	-3.168
568	N	ASP	65	-3.939	20.296	-2.440
570	CA	ASP	65	-3.409	19.158	-3.207
571	CB	ASP	65	-3.961	17.880	-2.587
572	CG	ASP	65	-3.129	16.657	-2.960
573	OD1	ASP	65	-1.912	16.755	-2.874
574	OD2	ASP	65	-3.722	15.600	-3.116
575	C	ASP	65	-3.880	19.277	-4.653
576	O	ASP	65	-4.968	18.808	-5.005
577	N	PHE	66	-3.050	19.893	-5.477
579	CA	PHE	66	-3.494	20.269	-6.821
580	CB	PHE	66	-4.181	21.629	-6.695
581	CG	PHE	66	-5.613	21.721	-7.222
582	CD1	PHE	66	-6.416	20.590	-7.277
583	CE1	PHE	66	-7.717	20.683	-7.752
584	CZ	PHE	66	-8.217	21.909	-8.172
585	CE2	PHE	66	-7.415	23.041	-8.118
586	CD2	PHE	66	-6.113	22.947	-7.643
587	C	PHE	66	-2.337	20.377	-7.812
588	O	PHE	66	-1.347	19.640	-7.747
589	N	CYS	67	-2.561	21.237	-8.791
591	CA	CYS	67	-1.571	21.560	-9.826
592	CB	CYS	67	-2.312	21.774	-11.140
593	SG	CYS	67	-3.226	20.341	-11.759
594	C	CYS	67	-0.645	22.773	-9.551
595	O	CYS	67	0.514	22.664	-9.967
596	N	PRO	68	-1.078	23.906	-8.989
597	CA	PRO	68	-0.109	24.980	-8.721
598	CB	PRO	68	-0.885	26.113	-8.125
599	CG	PRO	68	-2.351	25.727	-8.029
600	CD	PRO	68	-2.447	24.330	-8.616
601	C	PRO	68	1.012	24.535	-7.778
602	O	PRO	68	0.771	23.980	-6.702
603	N	PRO	69	2.231	24.787	-8.225
604	CA	PRO	69	3.439	24.392	-7.504
605	CB	PRO	69	4.555	24.571	-8.489
606	CG	PRO	69	4.025	25.281	-9.725

607	CD	PRO	69	2.533	25.445	-9.503
608	C	PRO	69	3.706	25.261	-6.280
609	O	PRO	69	3.349	26.443	-6.249
610	N	ALA	70	4.354	24.672	-5.290
612	CA	ALA	70	4.856	25.466	-4.159
613	CB	ALA	70	3.961	25.221	-2.950
614	C	ALA	70	6.309	25.120	-3.811
615	O	ALA	70	6.576	24.693	-2.679
616	N	PRO	71	7.255	25.506	-4.662
617	CA	PRO	71	8.610	24.941	-4.572
618	CB	PRO	71	9.249	25.253	-5.890
619	CG	PRO	71	8.358	26.208	-6.666
620	CD	PRO	71	7.097	26.373	-5.838
621	C	PRO	71	9.457	25.507	-3.429
622	O	PRO	71	10.352	24.812	-2.935
623	N	ASP	72	9.002	26.597	-2.831
625	CA	ASP	72	9.733	27.239	-1.734
626	CB	ASP	72	9.277	28.691	-1.633
627	CG	ASP	72	9.459	29.396	-2.975
628	OD1	ASP	72	10.596	29.691	-3.310
629	OD2	ASP	72	8.482	29.469	-3.709
630	C	ASP	72	9.479	26.539	-0.399
631	O	ASP	72	10.266	26.686	0.545
632	N	GLN	73	8.515	25.630	-0.392
634	CA	GLN	73	8.223	24.863	0.814
635	CB	GLN	73	6.791	24.343	0.714
636	CG	GLN	73	5.768	25.470	0.539
637	CD	GLN	73	5.306	26.071	1.870
638	OE1	GLN	73	4.161	25.855	2.285
639	NE2	GLN	73	6.160	26.870	2.487
642	C	GLN	73	9.197	23.698	0.972
643	O	GLN	73	9.472	23.314	2.114
644	N	ILE	74	9.939	23.397	-0.087
646	CA	ILE	74	10.915	22.303	-0.062
647	CB	ILE	74	11.453	22.127	-1.479
648	CG2	ILE	74	12.705	21.258	-1.491
649	CG1	ILE	74	10.383	21.558	-2.402
650	CD1	ILE	74	9.911	20.188	-1.931
651	C	ILE	74	12.084	22.586	0.874
652	O	ILE	74	12.374	21.751	1.739
653	N	ASP	75	12.518	23.837	0.916
655	CA	ASP	75	13.676	24.194	1.739
656	CB	ASP	75	14.085	25.627	1.420
657	CG	ASP	75	14.508	25.755	-0.040
658	OD1	ASP	75	15.667	25.482	-0.319
659	OD2	ASP	75	13.662	26.090	-0.859
660	C	ASP	75	13.331	24.091	3.216
661	O	ASP	75	13.863	23.201	3.895
662	N	ARG	76	12.180	24.659	3.538
664	CA	ARG	76	11.717	24.740	4.920
665	CB	ARG	76	10.475	25.618	4.901
666	CG	ARG	76	9.935	25.918	6.291
667	CD	ARG	76	8.634	26.701	6.173
668	NE	ARG	76	8.807	27.821	5.234
669	CZ	ARG	76	7.935	28.822	5.103
670	NH1	ARG	76	6.846	28.865	5.873
671	NH2	ARG	76	8.161	29.790	4.212
672	C	ARG	76	11.348	23.368	5.467
673	O	ARG	76	11.873	22.972	6.514
674	N	PHE	77	10.748	22.554	4.614

676	CA	PHE	77	10.268	21.240	5.032
677	CB	PHE	77	9.382	20.707	3.914
678	CG	PHE	77	8.430	19.598	4.334
679	CD1	PHE	77	8.884	18.293	4.474
680	CE1	PHE	77	8.006	17.290	4.860
681	CZ	PHE	77	6.673	17.595	5.102
682	CE2	PHE	77	6.219	18.900	4.964
683	CD2	PHE	77	7.098	19.902	4.581
684	C	PHE	77	11.424	20.274	5.267
685	O	PHE	77	11.458	19.614	6.316
686	N	VAL	78	12.473	20.408	4.473
688	CA	VAL	78	13.632	19.536	4.635
689	CB	VAL	78	14.473	19.615	3.367
690	CG1	VAL	78	15.853	19.014	3.576
691	CG2	VAL	78	13.757	18.939	2.202
692	C	VAL	78	14.455	19.929	5.856
693	O	VAL	78	14.808	19.037	6.638
694	N	GLN	79	14.423	21.203	6.209
696	CA	GLN	79	15.146	21.665	7.396
697	CB	GLN	79	15.285	23.178	7.277
698	CG	GLN	79	16.061	23.517	6.009
699	CD	GLN	79	16.031	25.015	5.719
700	OE1	GLN	79	14.984	25.590	5.394
701	NE2	GLN	79	17.208	25.613	5.755
704	C	GLN	79	14.416	21.280	8.686
705	O	GLN	79	15.067	20.794	9.622
706	N	ILE	80	13.097	21.183	8.602
708	CA	ILE	80	12.284	20.753	9.747
709	CB	ILE	80	10.817	20.972	9.397
710	CG2	ILE	80	9.919	20.421	10.499
711	CG1	ILE	80	10.516	22.443	9.152
712	CD1	ILE	80	9.114	22.627	8.579
713	C	ILE	80	12.488	19.270	10.043
714	O	ILE	80	12.862	18.908	11.167
715	N	VAL	81	12.518	18.467	8.992
717	CA	VAL	81	12.670	17.025	9.186
718	CB	VAL	81	12.057	16.315	7.982
719	CG1	VAL	81	11.958	14.814	8.221
720	CG2	VAL	81	10.663	16.866	7.705
721	C	VAL	81	14.139	16.643	9.406
722	O	VAL	81	14.412	15.635	10.075
723	N	ASP	82	15.048	17.551	9.078
725	CA	ASP	82	16.461	17.376	9.429
726	CB	ASP	82	17.326	18.363	8.648
727	CG	ASP	82	17.488	17.928	7.199
728	OD1	ASP	82	17.504	16.727	6.966
729	OD2	ASP	82	17.708	18.792	6.360
730	C	ASP	82	16.697	17.631	10.910
731	O	ASP	82	17.466	16.889	11.527
732	N	GLU	83	15.870	18.464	11.518
734	CA	GLU	83	16.013	18.745	12.946
735	CB	GLU	83	15.269	20.046	13.228
736	CG	GLU	83	15.349	20.464	14.690
737	CD	GLU	83	14.559	21.754	14.880
738	OE1	GLU	83	14.901	22.511	15.777
739	OE2	GLU	83	13.646	21.976	14.098
740	C	GLU	83	15.438	17.602	13.783
741	O	GLU	83	16.046	17.209	14.788
742	N	ALA	84	14.451	16.916	13.228
744	CA	ALA	84	13.871	15.755	13.911

745	CB	ALA	84	12.575	15.391	13.206
746	C	ALA	84	14.806	14.550	13.871
747	O	ALA	84	15.153	14.012	14.931
748	N	ASN	85	15.411	14.347	12.707
750	CA	ASN	85	16.353	13.237	12.467
751	CB	ASN	85	16.372	12.885	10.974
752	CG	ASN	85	15.164	12.053	10.524
753	OD1	ASN	85	15.204	10.815	10.530
754	ND2	ASN	85	14.154	12.735	10.018
757	C	ASN	85	17.791	13.547	12.906
758	O	ASN	85	18.686	12.721	12.693
759	N	ALA	86	18.024	14.735	13.447
761	CA	ALA	86	19.339	15.068	14.003
762	CB	ALA	86	19.559	16.574	13.918
763	C	ALA	86	19.378	14.625	15.458
764	O	ALA	86	20.445	14.404	16.043
765	N	ARG	87	18.191	14.498	16.024
767	CA	ARG	87	18.029	13.842	17.315
768	CB	ARG	87	17.136	14.699	18.198
769	CG	ARG	87	17.711	16.094	18.400
770	CD	ARG	87	16.802	16.924	19.298
771	NE	ARG	87	16.593	16.243	20.586
772	CZ	ARG	87	17.076	16.694	21.746
773	NH1	ARG	87	16.871	15.999	22.867
774	NH2	ARG	87	17.786	17.824	21.781
775	C	ARG	87	17.377	12.491	17.060
776	O	ARG	87	17.181	12.099	15.905
777	N	GLY	88	17.010	11.796	18.120
779	CA	GLY	88	16.302	10.521	17.947
780	C	GLY	88	14.805	10.710	18.177
781	O	GLY	88	14.192	10.003	18.983
782	N	GLU	89	14.226	11.672	17.477
784	CA	GLU	89	12.828	12.027	17.743
785	CB	GLU	89	12.716	13.531	17.973
786	CG	GLU	89	13.759	14.080	18.946
787	CD	GLU	89	13.797	13.327	20.275
788	OE1	GLU	89	14.897	12.949	20.657
789	OE2	GLU	89	12.739	13.072	20.833
790	C	GLU	89	11.940	11.641	16.570
791	O	GLU	89	12.284	11.894	15.410
792	N	ALA	90	10.773	11.102	16.880
794	CA	ALA	90	9.845	10.719	15.815
795	CB	ALA	90	8.736	9.857	16.394
796	C	ALA	90	9.269	11.946	15.115
797	O	ALA	90	8.989	12.982	15.737
798	N	VAL	91	9.166	11.840	13.804
800	CA	VAL	91	8.658	12.956	13.004
801	CB	VAL	91	9.792	13.517	12.152
802	CG1	VAL	91	10.618	12.419	11.497
803	CG2	VAL	91	9.305	14.542	11.133
804	C	VAL	91	7.457	12.546	12.158
805	O	VAL	91	7.563	11.827	11.152
806	N	GLY	92	6.315	13.060	12.572
808	CA	GLY	92	5.055	12.760	11.904
809	C	GLY	92	4.560	13.976	11.135
810	O	GLY	92	4.434	15.084	11.668
811	N	VAL	93	4.406	13.790	9.841
813	CA	VAL	93	3.872	14.873	9.021
814	CB	VAL	93	4.878	15.275	7.954
815	CG1	VAL	93	4.323	16.435	7.141

816	CG2	VAL	93	6.217	15.661	8.574
817	C	VAL	93	2.570	14.426	8.381
818	O	VAL	93	2.539	13.434	7.641
819	N	HIS	94	1.511	15.143	8.703
821	CA	HIS	94	0.194	14.792	8.202
822	CB	HIS	94	-0.779	14.660	9.372
823	CG	HIS	94	-1.184	15.959	10.035
824	ND1	HIS	94	-2.316	16.649	9.800
826	CE1	HIS	94	-2.336	17.748	10.579
827	NE2	HIS	94	-1.205	17.747	11.320
828	CD2	HIS	94	-0.487	16.649	10.998
829	C	HIS	94	-0.338	15.827	7.226
830	O	HIS	94	0.070	16.997	7.170
831	N	CYS	95	-1.251	15.341	6.417
833	CA	CYS	95	-2.046	16.220	5.574
834	CB	CYS	95	-1.582	16.100	4.130
835	SG	CYS	95	-1.201	14.431	3.563
836	C	CYS	95	-3.508	15.855	5.781
837	O	CYS	95	-3.951	15.736	6.927
838	N	ALA	96	-4.250	15.709	4.701
840	CA	ALA	96	-5.637	15.267	4.821
841	CB	ALA	96	-6.441	15.866	3.673
842	C	ALA	96	-5.736	13.746	4.769
843	O	ALA	96	-6.041	13.096	5.777
844	N	LEU	97	-5.350	13.195	3.629
846	CA	LEU	97	-5.541	11.761	3.364
847	CB	LEU	97	-6.061	11.618	1.938
848	CG	LEU	97	-7.424	12.274	1.757
849	CD1	LEU	97	-7.826	12.289	0.287
850	CD2	LEU	97	-8.485	11.578	2.603
851	C	LEU	97	-4.289	10.893	3.491
852	O	LEU	97	-4.369	9.692	3.221
853	N	GLY	98	-3.160	11.471	3.863
855	CA	GLY	98	-1.905	10.712	3.845
856	C	GLY	98	-1.423	10.513	2.406
857	O	GLY	98	-0.999	9.419	2.015
858	N	PHE	99	-1.469	11.594	1.641
860	CA	PHE	99	-1.251	11.547	0.182
861	CB	PHE	99	-2.616	11.474	-0.511
862	CG	PHE	99	-3.192	10.104	-0.885
863	CD1	PHE	99	-3.878	9.981	-2.086
864	CE1	PHE	99	-4.417	8.757	-2.460
865	CZ	PHE	99	-4.273	7.652	-1.632
866	CE2	PHE	99	-3.591	7.773	-0.428
867	CD2	PHE	99	-3.052	8.998	-0.056
868	C	PHE	99	-0.557	12.796	-0.380
869	O	PHE	99	-0.048	13.664	0.348
870	N	GLY	100	-0.417	12.749	-1.698
872	CA	GLY	100	-0.103	13.897	-2.577
873	C	GLY	100	1.075	14.775	-2.168
874	O	GLY	100	2.244	14.396	-2.322
875	N	ARG	101	0.729	15.928	-1.614
877	CA	ARG	101	1.686	16.936	-1.135
878	CB	ARG	101	0.927	17.888	-0.223
879	CG	ARG	101	-0.201	18.623	-0.920
880	CD	ARG	101	-1.283	18.948	0.098
881	NE	ARG	101	-1.896	17.700	0.576
882	CZ	ARG	101	-3.186	17.589	0.898
883	NH1	ARG	101	-3.956	18.677	0.959
884	NH2	ARG	101	-3.684	16.400	1.241

885	C	ARG	101	2.789	16.356	-0.269
886	O	ARG	101	3.971	16.474	-0.612
887	N	THR	102	2.407	15.540	0.697
889	CA	THR	102	3.390	15.105	1.682
890	CB	THR	102	2.679	14.825	2.994
891	OG1	THR	102	1.644	15.784	3.158
892	CG2	THR	102	3.654	14.984	4.147
893	C	THR	102	4.169	13.881	1.208
894	O	THR	102	5.317	13.690	1.626
895	N	GLY	103	3.672	13.246	0.157
897	CA	GLY	103	4.393	12.138	-0.478
898	C	GLY	103	5.542	12.723	-1.279
899	O	GLY	103	6.702	12.320	-1.116
900	N	THR	104	5.230	13.846	-1.901
902	CA	THR	104	6.198	14.624	-2.667
903	CB	THR	104	5.406	15.745	-3.332
904	OG1	THR	104	4.456	15.144	-4.200
905	CG2	THR	104	6.276	16.698	-4.141
906	C	THR	104	7.271	15.227	-1.762
907	O	THR	104	8.468	15.074	-2.041
908	N	MET	105	6.860	15.660	-0.581
910	CA	MET	105	7.804	16.223	0.387
911	CB	MET	105	7.004	16.865	1.511
912	CG	MET	105	6.267	18.112	1.045
913	SD	MET	105	7.320	19.480	0.521
914	CE	MET	105	6.036	20.703	0.184
915	C	MET	105	8.737	15.175	0.990
916	O	MET	105	9.949	15.417	1.065
917	N	LEU	106	8.240	13.964	1.181
919	CA	LEU	106	9.076	12.898	1.738
920	CB	LEU	106	8.159	11.785	2.234
921	CG	LEU	106	8.949	10.640	2.858
922	CD1	LEU	106	9.734	11.113	4.078
923	CD2	LEU	106	8.017	9.497	3.231
924	C	LEU	106	10.039	12.341	0.691
925	O	LEU	106	11.224	12.154	1.000
926	N	ALA	107	9.622	12.368	-0.565
928	CA	ALA	107	10.491	11.911	-1.651
929	CB	ALA	107	9.668	11.787	-2.928
930	C	ALA	107	11.629	12.893	-1.882
931	O	ALA	107	12.796	12.478	-1.891
932	N	CYS	108	11.323	14.173	-1.741
934	CA	CYS	108	12.341	15.206	-1.914
935	CB	CYS	108	11.642	16.542	-2.105
936	SG	CYS	108	12.748	17.934	-2.406
937	C	CYS	108	13.277	15.298	-0.712
938	O	CYS	108	14.475	15.541	-0.900
939	N	TYR	109	12.809	14.873	0.451
941	CA	TYR	109	13.672	14.839	1.633
942	CB	TYR	109	12.798	14.666	2.871
943	CG	TYR	109	13.600	14.590	4.165
944	CD1	TYR	109	14.169	15.746	4.682
945	CE1	TYR	109	14.911	15.689	5.851
946	CZ	TYR	109	15.085	14.477	6.503
947	OH	TYR	109	15.816	14.431	7.670
948	CE2	TYR	109	14.515	13.318	5.992
949	CD2	TYR	109	13.772	13.376	4.821
950	C	TYR	109	14.667	13.685	1.554
951	O	TYR	109	15.853	13.881	1.855
952	N	LEU	110	14.252	12.592	0.935

954	CA	LEU	110	15.150	11.449	0.760
955	CB	LEU	110	14.325	10.233	0.355
956	CG	LEU	110	13.330	9.830	1.438
957	CD1	LEU	110	12.394	8.732	0.941
958	CD2	LEU	110	14.044	9.397	2.714
959	C	LEU	110	16.191	11.738	-0.315
960	O	LEU	110	17.384	11.472	-0.104
961	N	VAL	111	15.799	12.500	-1.320
963	CA	VAL	111	16.768	12.884	-2.343
964	CB	VAL	111	16.050	13.510	-3.534
965	CG1	VAL	111	17.044	13.820	-4.649
966	CG2	VAL	111	14.951	12.599	-4.065
967	C	VAL	111	17.788	13.872	-1.788
968	O	VAL	111	18.968	13.511	-1.681
969	N	LYS	112	17.289	14.906	-1.131
971	CA	LYS	112	18.133	16.028	-0.706
972	CB	LYS	112	17.180	17.183	-0.414
973	CG	LYS	112	17.884	18.500	-0.111
974	CD	LYS	112	16.855	19.613	0.058
975	CE	LYS	112	17.500	20.951	0.399
976	NZ	LYS	112	16.473	21.985	0.600
977	C	LYS	112	18.991	15.749	0.529
978	O	LYS	112	20.076	16.325	0.655
979	N	GLU	113	18.579	14.836	1.393
981	CA	GLU	113	19.397	14.591	2.583
982	CB	GLU	113	18.529	14.748	3.822
983	CG	GLU	113	17.987	16.166	3.915
984	CD	GLU	113	19.126	17.184	3.998
985	OE1	GLU	113	20.005	16.998	4.829
986	OE2	GLU	113	19.035	18.179	3.292
987	C	GLU	113	20.068	13.226	2.605
988	O	GLU	113	21.094	13.067	3.275
989	N	ARG	114	19.526	12.261	1.882
991	CA	ARG	114	20.133 ·	10.929	1.913
992	CB	ARG	114	19.027	9.877	1.987
993	CG	ARG	114	18.007	10.100	3.109
994	CD	ARG	114	18.468	9.660	4.504
995	NE	ARG	114	19.401	10.604	5.145
996	CZ	ARG	114	19.035	11.496	6.069
997	NH1	ARG	114	19.929	12.362	6.549
998	NH2	ARG	114	17.764	11.557	6.473
999	C	ARG	114	20.981	10.678	0.673
1000	O	ARG	114	21.785	9.739	0.645
1001	N	GLY	115	20.796	11.510	-0.341
1003	CA	GLY	115	21.510	11.329	-1.609
1004	C	GLY	115	20.837	10.222	-2.414
1005	O	GLY	115	21.470	9.522	-3.214
1006	N	LEU	116	19.546	10.079	-2.178
1008	CA	LEU	116	18.772	8.997	-2.773
1009	CB	LEU	116	17.727	8.589	-1.744
1010	CG	LEU	116	16.894	7.413	-2.217
1011	CD1	LEU	116	17.791	6.206	-2.449
1012	CD2	LEU	116	15.804	7.092	-1.207
1013	C	LEU	116	18.073	9.479	-4.032
1014	O	LEU	116	17.284	10.424	-3.967
1015	N	ALA	117	18.279	8.782	-5.138
1017	CA	ALA	117	17.611	9.152	-6.394
1018	CB	ALA	117	17.987	8.151	-7.478
1019	C	ALA	117	16.095	9.176	-6.220
1020	O	ALA	117	15.533	8.384	-5.450

1021	N	ALA	118	15.436	9.995	-7.025
1023	CA	ALA	118	13.988	10.211	-6.878
1024	CB	ALA	118	13.582	11.375	-7.772
1025	C	ALA	118	13.158	8.978	-7.230
1026	O	ALA	118	12.188	8.680	-6.523
1027	N	GLY	119	13.708	8.131	-8.087
1029	CA	GLY	119	13.088	6.840	-8.399
1030	C	GLY	119	13.061	5.926	-7.175
1031	O	GLY	119	11.993	5.425	-6.807
1032	N	ASP	120	14.148	5.926	-6.418
1034	CA	ASP	120	14.251	5.042	-5.254
1035	CB	ASP	120	15.707	4.948	-4.815
1036	CG	ASP	120	16.663	4.621	-5.955
1037	OD1	ASP	120	17.707	5.261	-6.008
1038	OD2	ASP	120	16.324	3.788	-6.785
1039	C	ASP	120	13.448	5.601	-4.081
1040	O	ASP	120	12.790	4.829	-3.370
1041	N	ALA	121	13.314	6.918	-4.028
1043	CA	ALA	121	12.517	7.550	-2.975
1044	CB	ALA	121	12.743	9.056	-3.034
1045	C	ALA	121	11.037	7.244	-3.166
1046	O	ALA	121	10.409	6.689	-2.253
1047	N	ILE	122	10.594	7.289	-4.413
1049	CA	ILE	122	9.197	6.973	-4.717
1050	CB	ILE	122	8.869	7.495	-6.109
1051	CG2	ILE	122	7.440	7.144	-6.508
1052	CG1	ILE	122	9.065	8.999	-6.192
1053	CD1	ILE	122	8.752	9.479	-7.602
1054	C	ILE	122	8.919	5.472	-4.668
1055	O	ILE	122	7.833	5.088	-4.224
1056	N	ALA	123	9.935	4.647	-4.860
1058	CA	ALA	123	9.738	3.198	-4.754
1059	CB	ALA	123	10.936	2.490	-5.375
1060	C	ALA	123	9.582	2.754	-3.303
1061	O	ALA	123	8.662	1.985	-3.000
1062	N	GLU	124	10.257	3.447	-2.402
1064	CA	GLU	124	10.142	3.136	-0.975
1065	CB	GLU	124	11.335	3.773	-0.276
1066	CG	GLU	124	12.629	3.171	-0.810
1067	CD	GLU	124	13.834	3.993	-0.375
1068	OE1	GLU	124	13.702	4.737	0.586
1069	OE2	GLU	124	14.844	3.928	-1.066
1070	C	GLU	124	8.834	3.682	-0.410
1071	O	GLU	124	8.128	2.970	0.317
1072	N	ILE	125	8.393	4.785	-0.991
1074	CA	ILE	125	7.097	5.367	-0.647
1075	CB	ILE	125	7.051	6.755	-1.282
1076	CG2	ILE	125	5.634	7.296	-1.424
1077	CG1	ILE	125	7.924	7.721	-0.492
1078	CD1	ILE	125	7.832	9.129	-1.062
1079	C	ILE	125	5.942	4.500	-1.142
1080	O	ILE	125	5.103	4.112	-0.321
1081	N	ARG	126	6.119	3.899	-2.307
1083	CA	ARG	126	5.076	3.066	-2.908
1084	CB	ARG	126	5.407	2.931	-4.391
1085	CG	ARG	126	4.329	2.180	-5.161
1086	CD	ARG	126	2.960	2.828	-4.972
1087	NE	ARG	126	1.928	2.146	-5.771
1088	CZ	ARG	126	1.204	1.105	-5.349
1089	NH1	ARG	126	1.392	0.602	-4.126

1090	NH2	ARG	126	0.283	0.568	-6.151
1091	C	ARG	126	4.976	1.688	-2.251
1092	O	ARG	126	3.871	1.139	-2.172
1093	N	ARG	127	6.031	1.259	-1.574
1095	CA	ARG	127	5.951	0.002	-0.827
1096	CB	ARG	127	7.340	-0.599	-0.665
1097	CG	ARG	127	7.992	-0.873	-2.013
1098	CD	ARG	127	9.253	-1.709	-1.840
1099	NE	ARG	127	10.083	-1.187	-0.744
1100	CZ	ARG	127	11.278	-0.622	-0.922
1101	NH1	ARG	127	11.739	-0.405	-2.156
1102	NH2	ARG	127	11.981	-0.212	0.135
1103	C	ARG	127	5.323	0.199	0.551
1104	O	ARG	127	4.970	-0.785	1.212
1105	N	LEU	128	5.150	1.443	0.966
1107	CA	LEU	128	4.425	1.710	2.207
1108	CB	LEU	128	5.111	2.827	2.998
1109	CG	LEU	128	6.092	2.324	4.058
1110	CD1	LEU	128	5.422	1.304	4.972
1111	CD2	LEU	128	7.379	1.752	3.473
1112	C	LEU	128	2.978	2.110	1.920
1113	O	LEU	128	2.077	1.727	2.679
1114	N	ARG	129	2.761	2.777	0.793
1116	CA	ARG	129	1.427	3.293	0.438
1117	CB	ARG	129	1.031	4.282	1.537
1118	CG	ARG	129	-0.411	4.773	1.494
1119	CD	ARG	129	-0.591	5.850	2.558
1120	NE	ARG	129	-1.998	6.222	2.754
1121	CZ	ARG	129	-2.534	6.300	3.974
1122	NH1	ARG	129	-1.803	5.970	5.040
1123	NH2	ARG	129	-3.810	6.660	4.124
1124	C	ARG	129	1.450	4.008	-0.923
1125	O	ARG	129	2.368	4.778	-1.228
1126	N	PRO	130	0.469	3.706	-1.756
1127	CA	PRO	130	0.213	4.511	-2.959
1128	CB	PRO	130	-0.828	3.738	-3.711
1129	CG	PRO	130	-1.370	2.628	-2.821
1130	CD	PRO	130	-0.549	2.674	-1.544
1131	C	PRO	130	-0.326	5.908	-2.632
1132	O	PRO	130	-0.940	6.120	-1.580
1133	N	GLY	131	-0.088	6.856	-3.526
1135	CA	GLY	131	-0.756	8.161	-3.404
1136	C	GLY	131	0.130	9.399	-3.532
1137	O	GLY	131	0.387	10.084	-2.535
1138	N	SER	132	0.443	9.765	-4.765
1140	CA	SER	132	1.174	11.013	-5.045
1141	CB	SER	132	2.674	10.743	-5.102
1142	OG	SER	132	3.106	10.386	-3.795
1143	C	SER	132	0.702	11.627	-6.364
1144	O	SER	132	0.463	10.910	-7.342
1145	N	ILE	133	0.544	12.940	-6.372
1147	CA	ILE	133	0.050	13.633	-7.571
1148	CB	ILE	133	-0.575	14.966	-7.146
1149	CG2	ILE	133	-0.945	15.872	-8.318
1150	CG1	ILE	133	-1.815	14.721	-6.301
1151	CD1	ILE	133	-2.665	15.984	-6.247
1152	C	ILE	133	1.173	13.830	-8.589
1153	O	ILE	133	2.241	14.357	-8.258
1154	N	GLU	134	0.858	13.565	-9.851
1156	CA	GLU	134	1.848	13.637	-10.935

1157	CB	GLU	134	1.226	13.055	-12.197
1158	CG	GLU	134	0.892	11.578	-12.033
1159	CD	GLU	134	0.188	11.072	-13.288
1160	OE1	GLU	134	0.284	11.753	-14.299
1161	OE2	GLU	134	-0.574	10.124	-13.159
1162	C	GLU	134	2.338	15.052	-11.246
1163	O	GLU	134	3.504	15.195	-11.627
1164	N	THR	135	1.612	16.071	-10.814
1166	CA	THR	135	2.082	17.439	-11.029
1167	CB	THR	135	0.925	18.406	-10.834
1168	OG1	THR	135	-0.146	18.009	-11.678
1169	CG2	THR	135	1.340	19.819	-11.219
1170	C	THR	135	3.200	17.777	-10.045
1171	O	THR	135	4.247	18.269	-10.482
1172	N	TYR	136	3.145	17.168	-8.871
1174	CA	TYR	136	4.200	17.364	-7.872
1175	CB	TYR	136	3.647	17.007	-6.503
1176	CG	TYR	136	2.593	17.957	-5.958
1177	CD1	TYR	136	2.754	19.331	-6.085
1178	CE1	TYR	136	1.784	20.192	-5.589
1179	CZ	TYR	136	0.662	19.673	-4.956
1180	OH	TYR	136	-0.365	20.508	-4.586
1181	CE2	TYR	136	0.514	18.302	-4.802
1182	CD2	TYR	136	1.484	17.443	-5.299
1183	C	TYR	136	5.406	16.470	-8.149
1184	O	TYR	136	6.541	16.839	-7.813
1185	N	GLU	137	5.180	15.442	-8.952
1187	CA	GLU	137	6.265	14.549	-9.349
1188	CB	GLU	137	5.719	13.155	-9.656
1189	CG	GLU	137	4.785	12.608	-8.578
1190	CD	GLU	137	5.422	12.575	-7.186
1191	OE1	GLU	137	6.135	11.623	-6.914
1192	OE2	GLU	137	4.977	13.366	-6.368
1193	C	GLU	137	6.973	15.096	-10.588
1194	O	GLU	137	8.138	14.762	-10.831
1195	N	GLN	138	6.334	16.009	-11.297
1197	CA	GLN	138	7.038	16.697	-12.375
1198	CB	GLN	138	6.020	17.242	-13.378
1199	CG	GLN	138	6.593	17.418	-14.789
1200	CD	GLN	138	7.711	18.459	-14.852
1201	OE1	GLN	138	7.527	19.615	-14.453
1202	NE2	GLN	138	8.856	18.036	-15.359
1205	C	GLN	138	7.830	17.832	-11.744
1206	O	GLN	138	9.028	17.975	-12.020
1207	N	GLU	139	7.235	18.401	-10.710
1209	CA	GLU	139	7.822	19.523	-9.979
1210	CB	GLU	139	6.784	20.076	-9.008
1211	CG	GLU	139	5.631	20.789	-9.694
1212	CD	GLU	139	4.577	21.116	-8.643
1213	OE1	GLU	139	3.406	20.882	-8.904
1214	OE2	GLU	139	4.978	21.486	-7.547
1215	C	GLU	139	9.066	19.204	-9.155
1216	O	GLU	139	9.860	18.291	-9.445
1217	N	LYS	140	9.013	19.819	-7.986
1219	CA	LYS	140	10.132	20.030	-7.062
1220	CB	LYS	140	9.556	21.013	-6.045
1221	CG	LYS	140	8.214	20.466	-5.559
1222	CD	LYS	140	7.437	21.413	-4.657
1223	CE	LYS	140	6.136	20.760	-4.204
1224	NZ	LYS	140	5.352	21.653	-3.340

1225	C	LYS	140	10.659	18.811	-6.308
1226	O	LYS	140	11.628	18.950	-5.556
1227	N	ALA	141	10.067	17.644	-6.490
1229	CA	ALA	141	10.575	16.481	-5.770
1230	CB	ALA	141	9.434	15.828	-5.018
1231	C	ALA	141	11.189	15.445	-6.686
1232	O	ALA	141	12.180	14.800	-6.321
1233	N	VAL	142	10.646	15.313	-7.882
1235	CA	VAL	142	11.112	14.219	-8.731
1236	CB	VAL	142	9.960	13.276	-9.049
1237	CG1	VAL	142	10.451	12.006	-9.744
1238	CG2	VAL	142	9.205	12.915	-7.777
1239	C	VAL	142	11.793	14.739	-9.985
1240	O	VAL	142	13.010	14.930	-9.941
1241	N	PHE	143	11.039	15.138	-10.999
1243	CA	PHE	143	11.676	15.455	-12.282
1244	CB	PHE	143	10.634	15.597	-13.382
1245	CG	PHE	143	9.954	14.292	-13.786
1246	CD1	PHE	143	8.636	14.302	-14.227
1247	CE1	PHE	143	8.014	13.113	-14.588
1248	CZ	PHE	143	8.712	11.913	-14.515
1249	CE2	PHE	143	10.034	11.906	-14.087
1250	CD2	PHE	143	10.656	13.095	-13.727
1251	C	PHE	143	12.546	16.705	-12.210
1252	O	PHE	143	13.767	16.565	-12.358
1253	N	GLN	144	12.013	17.787	-11.663
1255	CA	GLN	144	12.795	19.027	-11.582
1256	CB	GLN	144	11.858	20.182	-11.266
1257	CG	GLN	144	10.866	20.430	-12.392
1258	CD	GLN	144	9.865	21.499	-11.970
1259	OE1	GLN	144	9.977	22.066	-10.877
1260	NE2	GLN	144	8.789	21.612	-12.730
1263	C	GLN	144	13.899	18.976	-10.530
1264	O	GLN	144	14.992	19.499	-10.780
1265	N	PHE	145	13.747	18.123	-9.530
1267	CA	PHE	145	14.789	18.046	-8.507
1268	CB	PHE	145	14.174	17.614	-7.185
1269	CG	PHE	145	15.117	17.799	-6.002
1270	CD1	PHE	145	16.060	18.817	-6.028
1271	CE1	PHE	145	16.928	18.993	-4.959
1272	CZ	PHE	145	16.852	18.147	-3.862
1273	CE2	PHE	145	15.912	17.125	-3.839
1274	CD2	PHE	145	15.046	16.948	-4.910
1275	C	PHE	145	15.896	17.074	-8.921
1276	O	PHE	145	17.066	17.324	-8.618
1277	N	TYR	146	15.575	16.155	-9.813
1279	CA	TYR	146	16.572	15.226	-10.339
1280	CB	TYR	146	15.851	13.970	-10.831
1281	CG	TYR	146	16.737	12.742	-10.981
1282	CD1	TYR	146	17.740	12.497	-10.051
1283	CE1	TYR	146	18.546	11.372	-10.179
1284	CZ	TYR	146	18.343	10.493	-11.234
1285	OH	TYR	146	19.139	9.376	-11.360
1286	CE2	TYR	146	17.339	10.735	-12.163
1287	CD2	TYR	146	16.533	11.860	-12.034
1288	C	TYR	146	17.338	15.873	-11.489
1289	O	TYR	146	18.529	15.599	-11.669
1290	N	GLN	147	16.746	16.906	-12.070
1292	CA	GLN	147	17.453	17.732	-13.054
1293	CB	GLN	147	16.406	18.449	-13.901

1294	CG	GLN	147	15.549	17.427	-14.643
1295	CD	GLN	147	14.345	18.080	-15.314
1296	OE1	GLN	147	13.487	18.690	-14.663
1297	NE2	GLN	147	14.234	17.837	-16.608
1300	C	GLN	147	18.362	18.738	-12.344
1301	O	GLN	147	19.451	19.052	-12.841
1302	N	ARG	148	18.048	18.993	-11.083
1304	CA	ARG	148	18.876	19.832	-10.213
1305	CB	ARG	148	17.949	20.396	-9.142
1306	CG	ARG	148	18.542	21.580	-8.392
1307	CD	ARG	148	17.557	22.055	-7.335
1308	NE	ARG	148	16.198	22.087	-7.900
1309	CZ	ARG	148	15.087	22.121	-7.160
1310	NH1	ARG	148	15.170	22.258	-5.835
1311	NH2	ARG	148	13.890	22.094	-7.754
1312	C	ARG	148	19.999	19.011	-9.562
1313	O	ARG	148	21.002	19.576	-9.109
1314	N	THR	149	19.942	17.699	-9.743
1316	CA	THR	149	20.972	16.781	-9.236
1317	CB	THR	149	20.338	15.401	-9.049
1318	OG1	THR	149	19.179	15.553	-8.246
1319	CG2	THR	149	21.258	14.404	-8.349
1320	C	THR	149	22.159	16.691	-10.204
1321	O	THR	149	23.207	16.135	-9.856
1322	N	LYS	150	22.064	17.412	-11.313
1324	CA	LYS	150	23.145	17.484	-12.303
1325	CB	LYS	150	22.552	18.209	-13.509
1326	CG	LYS	150	23.565	18.460	-14.618
1327	CD	LYS	150	23.042	19.495	-15.608
1328	CE	LYS	150	22.778	20.830	-14.914
1329	NZ	LYS	150	24.010	21.383	-14.325
1330	C	LYS	150	24.372	18.264	-11.805
1331	O	LYS	150	25.484	18.044	-12.301
1332	N	GLU	151	24.202	19.068	-10.767
1334	CA	GLU	151	25.341	19.791	-10.190
1335	CB	GLU	151	24.824	21.021	-9.441
1336	CG	GLU	151	23.695	20.691	-8.469
1337	CD	GLU	151	23.111	21.967	-7.872
1338	OE1	GLU	151	23.517	22.322	-6.775
1339	OE2	GLU	151	22.311	22.593	-8.553
1340	C	GLU	151	26.191	18.878	-9.295
1341	O	GLU	151	26.041	18.951	-8.083
1342	OXT	GLU	151	27.093	18.256	-9.838

Table X

Atom No	Atom name	Residue	Residue No	x coord	y coord	z coord
1271	N	PRO	159	7.810	59.922	28.682
1272	CA	PRO	159	7.834	60.673	27.424
1273	CB	PRO	159	6.519	61.385	27.362
1274	CG	PRO	159	5.766	61.156	28.664
1275	CD	PRO	159	6.652	60.259	29.513
1276	C	PRO	159	9.003	61.649	27.419
1277	O	PRO	159	9.148	62.480	28.324
1278	N	THR	160	9.817	61.560	26.386
1279	CA	THR	160	11.063	62.328	26.377
1280	CB	THR	160	12.168	61.440	25.831
1281	OG1	THR	160	12.161	60.233	26.582
1282	CG2	THR	160	13.525	62.113	25.990
1283	C	THR	160	10.970	63.589	25.534
1284	O	THR	160	10.738	63.526	24.323
1285	N	ARG	161	11.150	64.726	26.181
1286	CA	ARG	161	11.183	66.001	25.462
1288	CB	ARG	161	11.339	67.120	26.484
1289	CG	ARG	161	11.208	68.500	25.851
1290	CD	ARG	161	11.629	69.598	26.819
1291	NE	ARG	161	13.058	69.463	27.148
1292	CZ	ARG	161	13.521	69.226	28.379
1293	NH1	ARG	161	12.672	69.116	29.403
1294	NH2	ARG	161	14.834	69.100	28.583
1295	C	ARG	161	12.376	66.009	24.511
1296	O	ARG	161	13.487	65.624	24.893
1297	N	ILE	162	12.111	66.309	23.252
1298	CA	ILE	162	13.177	66.368	22.253
1300	CB	ILE	162	12.753	65.567	21.024
1301	CG2	ILE	162	13.842	65.603	19.958
1302	CG1	ILE	162	12.418	64.122	21.382
1303	CD1	ILE	162	13.635	63.356	21.892
1304	C	ILE	162	13.402	67.823	21.869
1305	O	ILE	162	14.536	68.281	21.682
1306	N	LEU	163	12.300	68.549	21.819
1307	CA	LEU	163	12.333	69.988	21.536
1309	CB	LEU	163	11.808	70.243	20.122
1310	CG	LEU	163	12.835	69.894	19.050
1311	CD1	LEU	163	12.244	70.054	17.656
1312	CD2	LEU	163	14.079	70.762	19.197
1313	C	LEU	163	11.466	70.721	22.550
1314	O	LEU	163	10.632	70.092	23.213
1315	N	PRO	164	11.703	72.012	22.725
1316	CA	PRO	164	10.737	72.843	23.446
1317	CB	PRO	164	11.263	74.242	23.358
1318	CG	PRO	164	12.565	74.238	22.571
1319	CD	PRO	164	12.804	72.796	22.156
1320	C	PRO	164	9.354	72.708	22.817
1321	O	PRO	164	9.170	72.931	21.615
1322	N	ASN	165	8.421	72.281	23.654
1323	CA	ASN	165	7.035	71.973	23.265
1325	CB	ASN	165	6.370	73.188	22.628
1326	CG	ASN	165	6.228	74.328	23.628
1327	OD1	ASN	165	5.554	74.179	24.654
1328	ND2	ASN	165	6.774	75.473	23.259
1329	C	ASN	165	6.920	70.781	22.313
1332	O	ASN	165	6.005	70.751	21.479
1333	N	LEU	166	7.743	69.766	22.528
1334	CA	LEU	166	7.694	68.542	21.715
1336	CB	LEU	166	8.507	68.743	20.438
1337	CG	LEU	166	8.613	67.459	19.613

1339	CD1	LEU	166	7.243	66.934	19.198
1340	CD2	LEU	166	9.495	67.656	18.386
1341	C	LEU	166	8.242	67.343	22.489
1342	O	LEU	166	9.458	67.203	22.685
1343	N	TYR	167	7.326	66.479	22.889
1345	CA	TYR	167	7.661	65.244	23.606
1346	CB	TYR	167	6.751	65.099	24.825
1347	CG	TYR	167	7.047	66.005	26.019
1348	CD1	TYR	167	6.568	67.309	26.051
1349	CE1	TYR	167	6.835	68.120	27.149
1350	CZ	TYR	167	7.573	67.620	28.213
1351	OH	TYR	167	7.776	68.406	29.326
1352	CE2	TYR	167	8.046	66.316	28.186
1353	CD2	TYR	167	7.779	65.508	27.090
1354	C	TYR	167	7.477	64.016	22.714
1355	O	TYR	167	6.441	63.841	22.060
1356	N	LEU	168	8.487	63.166	22.723
1358	CA	LEU	168	8.456	61.889	22.009
1359	CB	LEU	168	9.904	61.458	21.802
1360	CG	LEU	168	10.031	60.174	20.994
1361	CD1	LEU	168	9.446	60.354	19.600
1362	CD2	LEU	168	11.490	59.745	20.909
1363	C	LEU	168	7.727	60.843	22.848
1364	O	LEU	168	8.101	60.587	24.002
1365	N	GLY	169	6.710	60.237	22.261
1367	CA	GLY	169	5.895	59.257	22.975
1368	C	GLY	169	5.992	57.843	22.405
1369	O	GLY	169	5.272	57.451	21.476
1370	N	CYS	170	6.877	57.075	23.011
1372	CA	CYS	170	6.962	55.637	22.743
1373	CB	CYS	170	8.266	55.120	23.348
1374	SG	CYS	170	8.700	53.387	23.049
1375	C	CYS	170	5.772	54.968	23.422
1376	O	CYS	170	5.354	55.430	24.490
1377	N	GLN	171	5.388	53.797	22.933
1379	CA	GLN	171	4.230	53.025	23.430
1380	CB	GLN	171	4.108	51.825	22.499
1381	CG	GLN	171	5.387	50.998	22.578
1382	CD	GLN	171	5.407	49.864	21.564
1383	OE1	GLN	171	6.432	49.650	20.907
1384	NE2	GLN	171	4.271	49.211	21.394
1387	C	GLN	171	4.332	52.480	24.867
1388	O	GLN	171	3.398	51.816	25.329
1389	N	ARG	172	5.436	52.731	25.555
1391	CA	ARG	172	5.604	52.289	26.939
1392	CB	ARG	172	7.038	51.800	27.117
1393	CG	ARG	172	7.400	50.730	26.092
1394	CD	ARG	172	6.526	49.488	26.229
1395	NE	ARG	172	6.825	48.529	25.157
1396	CZ	ARG	172	6.807	47.207	25.336
1397	NH1	ARG	172	6.506	46.701	26.535
1398	NH2	ARG	172	7.090	46.392	24.318
1399	C	ARG	172	5.342	53.446	27.903
1400	O	ARG	172	5.244	53.239	29.119
1401	N	ASP	173	5.183	54.637	27.348
1403	CA	ASP	173	4.962	55.838	28.160
1404	CB	ASP	173	5.188	57.086	27.313
1405	CG	ASP	173	6.621	57.152	26.808
1406	OD1	ASP	173	7.488	56.556	27.438
1407	OD2	ASP	173	6.857	57.886	25.856
1408	C	ASP	173	3.558	55.868	28.742
1409	O	ASP	173	2.586	55.445	28.105
1410	N	VAL	174	3.467	56.365	29.962
1412	CA	VAL	174	2.163	56.446	30.630
1413	CB	VAL	174	2.373	56.566	32.139

1414	CG1	VAL	174	1.055	56.735	32.891
1415	CG2	VAL	174	3.125	55.356	32.675
1416	C	VAL	174	1.364	57.639	30.113
1417	O	VAL	174	1.762	58.797	30.283
1418	N	LEU	175	0.206	57.346	29.543
1420	CA	LEU	175	−0.702	58.394	29.049
1421	CB	LEU	175	−1.527	57.836	27.897
1422	CG	LEU	175	−0.675	57.638	26.651
1423	CD1	LEU	175	−1.479	56.974	25.540
1424	CD2	LEU	175	−0.108	58.972	26.178
1425	C	LEU	175	−1.645	58.911	30.134
1426	O	LEU	175	−2.867	58.748	30.049
1427	N	ASN	176	−1.067	59.505	31.162
1429	CA	ASN	176	−1.863	60.067	32.249
1430	CB	ASN	176	−1.081	59.893	33.548
1431	CG	ASN	176	−1.887	60.398	34.738
1432	OD1	ASN	176	−1.914	61.603	35.013
1433	ND2	ASN	176	−2.584	59.485	35.390
1436	C	ASN	176	−2.126	61.537	31.950
1437	O	ASN	176	−1.178	62.322	31.834
1438	N	LYS	177	−3.386	61.939	31.994
1440	CA	LYS	177	−3.742	63.305	31.584
1441	CB	LYS	177	−5.253	63.389	31.401
1442	CG	LYS	177	−5.678	64.803	31.020
1443	CD	LYS	177	−7.140	64.870	30.596
1444	CE	LYS	177	−7.372	64.142	29.277
1445	NZ	LYS	177	−8.756	64.328	28.811
1446	C	LYS	177	−3.261	64.383	32.556
1447	O	LYS	177	−2.667	65.360	32.080
1448	N	GLU	178	−3.132	64.034	33.827
1450	CA	GLU	178	−2.633	64.996	34.812
1451	CB	GLU	178	−2.907	64.469	36.214
1452	CG	GLU	178	−2.362	65.422	37.273
1453	CD	GLU	178	−2.326	64.727	38.627
1454	OE1	GLU	178	−2.944	63.675	38.737
1455	OE2	GLU	178	−1.735	65.281	39.546
1456	C	GLU	178	−1.130	65.173	34.651
1457	O	GLU	178	−0.668	66.316	34.563
1458	N	LEU	179	−0.466	64.094	34.269
1460	CA	LEU	179	0.980	64.110	34.041
1461	CB	LEU	179	1.442	62.650	34.005
1462	CG	LEU	179	2.927	62.451	33.702
1463	CD1	LEU	179	3.498	61.304	34.528
1464	CD2	LEU	179	3.183	62.216	32.213
1465	C	LEU	179	1.329	64.845	32.748
1466	O	LEU	179	2.333	65.571	32.712
1467	N	MET	180	0.413	64.856	31.796
1469	CA	MET	180	0.649	65.614	30.571
1470	CB	MET	180	−0.261	65.095	29.465
1471	CG	MET	180	0.038	63.631	29.162
1472	SD	MET	180	−0.821	62.933	27.733
1473	CE	MET	180	−2.525	63.329	28.179
1474	C	MET	180	0.410	67.099	30.810
1475	O	MET	180	1.274	67.904	30.439
1476	N	GLN	181	−0.508	67.410	31.710
1478	CA	GLN	181	−0.753	68.808	32.077
1479	CB	GLN	181	−2.083	68.880	32.818
1480	CG	GLN	181	−3.225	68.380	31.940
1481	CD	GLN	181	−4.522	68.322	32.740
1482	OE1	GLN	181	−4.974	67.247	33.159
1483	NE2	GLN	181	−5.108	69.488	32.939
1486	C	GLN	181	0.362	69.363	32.966
1487	O	GLN	181	0.765	70.515	32.774
1488	N	GLN	182	1.029	68.482	33.697
1490	CA	GLN	182	2.188	68.872	34.513

1491	CB	GLN	182	2.373	67.811	35.590
1492	CG	GLN	182	1.165	67.769	36.517
1493	CD	GLN	182	1.232	66.556	37.438
1494	OE1	GLN	182	0.810	65.449	37.075
1495	NE2	GLN	182	1.696	66.796	38.650
1498	C	GLN	182	3.479	68.994	33.700
1499	O	GLN	182	4.458	69.573	34.183
1500	N	ASN	183	3.465	68.490	32.477
1502	CA	ASN	183	4.597	68.659	31.560
1503	CB	ASN	183	4.841	67.355	30.804
1504	CG	ASN	183	5.774	66.424	31.582
1505	OD1	ASN	183	6.998	66.487	31.420
1506	ND2	ASN	183	5.195	65.551	32.387
1509	C	ASN	183	4.345	69.797	30.571
1510	O	ASN	183	5.234	70.153	29.787
1511	N	GLY	184	3.136	70.340	30.600
1513	CA	GLY	184	2.778	71.482	29.753
1514	C	GLY	184	2.211	71.046	28.406
1515	O	GLY	184	2.220	71.826	27.445
1516	N	ILE	185	1.753	69.807	28.340
1518	CA	ILE	185	1.241	69.238	27.090
1519	CB	ILE	185	1.373	67.717	27.164
1520	CG2	ILE	185	0.772	67.030	25.942
1521	CG1	ILE	185	2.837	67.322	27.322
1522	CD1	ILE	185	3.009	65.809	27.389
1523	C	ILE	185	−0.206	69.655	26.863
1524	O	ILE	185	−1.093	69.385	27.685
1525	N	GLY	186	−0.429	70.291	25.727
1527	CA	GLY	186	−1.752	70.800	25.376
1528	C	GLY	186	−2.207	70.187	24.062
1529	O	GLY	186	−3.407	70.157	23.753
1530	N	TYR	187	−1.239	69.767	23.267
1532	CA	TYR	187	−1.544	69.081	22.011
1533	CB	TYR	187	−0.900	69.854	20.863
1534	CG	TYR	187	−1.538	71.217	20.579
1535	CD1	TYR	187	−1.014	72.377	21.140
1536	CE1	TYR	187	−1.600	73.607	20.873
1537	CZ	TYR	187	−2.710	73.675	20.042
1538	OH	TYR	187	−3.299	74.893	19.786
1539	CE2	TYR	187	−3.233	72.522	19.476
1540	CD2	TYR	187	−2.645	71.294	19.745
1541	C	TYR	187	−1.053	67.634	22.050
1542	O	TYR	187	0.029	67.340	22.571
1543	N	VAL	188	−1.887	66.726	21.576
1545	CA	VAL	188	−1.518	65.303	21.553
1546	CB	VAL	188	−2.387	64.524	22.540
1547	CG1	VAL	188	−2.002	63.048	22.553
1548	CG2	VAL	188	−2.292	65.097	23.950
1549	C	VAL	188	−1.680	64.717	20.151
1550	O	VAL	188	−2.798	64.541	19.650
1551	N	LEU	189	−0.558	64.351	19.563
1553	CA	LEU	189	−0.536	63.798	18.210
1554	CB	LEU	189	0.669	64.417	17.504
1555	CG	LEU	189	0.605	64.373	15.979
1556	CD1	LEU	189	1.550	65.408	15.384
1557	CD2	LEU	189	0.899	62.991	15.407
1558	C	LEU	189	−0.410	62.278	18.301
1559	O	LEU	189	0.602	61.751	18.775
1560	N	ASN	190	−1.431	61.581	17.841
1562	CA	ASN	190	−1.420	60.121	17.902
1563	CB	ASN	190	−2.760	59.630	18.441
1564	CG	ASN	190	−2.789	58.109	18.367
1565	OD1	ASN	190	−3.450	57.533	17.495
1566	ND2	ASN	190	−1.926	57.480	19.143
1569	C	ASN	190	−1.139	59.514	16.529

1570	O	ASN	190	−1.955	59.608	15.606
1571	N	ALA	191	−0.025	58.806	16.447
1573	CA	ALA	191	0.407	58.172	15.194
1574	CB	ALA	191	1.908	58.389	15.046
1575	C	ALA	191	0.112	56.670	15.130
1576	O	ALA	191	0.899	55.919	14.542
1577	N	SER	192	−0.958	56.224	15.766
1579	CA	SER	192	−1.206	54.782	15.854
1580	CB	SER	192	−1.912	54.479	17.170
1581	OG	SER	192	−1.059	54.926	18.225
1582	C	SER	192	−1.992	54.260	14.649
1583	O	SER	192	−2.502	55.028	13.822
1584	N	ASN	193	−1.985	52.944	14.516
1586	CA	ASN	193	−2.607	52.290	13.363
1587	CB	ASN	193	−2.303	50.793	13.362
1588	CG	ASN	193	−2.461	50.148	14.738
1589	OD1	ASN	193	−3.403	50.423	15.490
1590	ND2	ASN	193	−1.525	49.268	15.045
1593	C	ASN	193	−4.102	52.546	13.265
1594	O	ASN	193	−4.865	52.431	14.231
1595	N	THR	194	−4.471	52.920	12.050
1597	CA	THR	194	−5.833	53.284	11.624
1598	CB	THR	194	−6.594	52.008	11.267
1599	OG1	THR	194	−6.679	51.178	12.419
1600	CG2	THR	194	−5.879	51.224	10.172
1601	C	THR	194	−6.628	54.102	12.643
1602	O	THR	194	−7.778	53.767	12.949
1603	N	CYS	195	−6.038	55.184	13.127
1605	CA	CYS	195	−6.763	56.090	14.023
1606	CB	CYS	195	−5.924	56.299	15.279
1607	SG	CYS	195	−5.598	54.819	16.262
1608	C	CYS	195	−6.992	57.434	13.342
1609	O	CYS	195	−6.096	58.279	13.351
1610	N	PRO	196	−8.127	57.602	12.686
1611	CA	PRO	196	−8.392	58.842	11.953
1612	CB	PRO	196	−9.475	58.481	10.984
1613	CG	PRO	196	−10.070	57.140	11.389
1614	CD	PRO	196	−9.222	56.638	12.548
1615	C	PRO	196	−8.853	59.980	12.862
1616	O	PRO	196	−9.020	59.801	14.074
1617	N	LYS	197	−8.872	61.162	12.264
1619	CA	LYS	197	−9.517	62.397	12.769
1620	CB	LYS	197	−11.033	62.207	12.961
1621	CG	LYS	197	−11.443	61.549	14.278
1622	CD	LYS	197	−12.955	61.388	14.391
1623	CE	LYS	197	−13.667	62.736	14.402
1624	NZ	LYS	197	−15.125	62.567	14.529
1625	C	LYS	197	−8.890	63.026	14.018
1626	O	LYS	197	−8.593	62.383	15.033
1627	N	PRO	198	−8.633	64.316	13.884
1628	CA	PRO	198	−8.458	65.184	15.049
1629	CB	PRO	198	−8.097	66.522	14.486
1630	CG	PRO	198	−8.299	66.495	12.979
1631	CD	PRO	198	−8.726	65.078	12.637
1632	C	PRO	198	−9.747	65.276	15.861
1633	O	PRO	198	−10.852	65.161	15.319
1634	N	ASP	199	−9.590	65.480	17.156
1636	CA	ASP	199	−10.746	65.583	18.054
1637	CB	ASP	199	−11.299	64.182	18.311
1638	CG	ASP	199	−12.690	64.271	18.937
1639	OD1	ASP	199	−13.012	63.414	19.745
1640	OD2	ASP	199	−13.391	65.220	18.610
1641	C	ASP	199	−10.340	66.243	19.372
1642	O	ASP	199	−9.345	65.861	19.998

1643	N	PHE	200	-11.089	67.256	19.774
1645	CA	PHE	200	-10.774	67.952	21.027
1646	CB	PHE	200	-11.397	69.344	20.991
1647	CG	PHE	200	-11.066	70.229	22.194
1648	CD1	PHE	200	-12.007	71.133	22.672
1649	CE1	PHE	200	-11.703	71.942	23.759
1650	CZ	PHE	200	-10.460	71.848	24.370
1651	CE2	PHE	200	-9.521	70.942	23.896
1652	CD2	PHE	200	-9.825	70.134	22.809
1653	C	PHE	200	-11.306	67.178	22.231
1654	O	PHE	200	-12.516	67.115	22.468
1655	N	ILE	201	-10.386	66.576	22.964
1657	CA	ILE	201	-10.736	65.876	24.200
1658	CB	ILE	201	-10.063	64.506	24.191
1659	CG2	ILE	201	-10.399	63.709	25.447
1660	CG1	ILE	201	-10.483	63.723	22.950
1661	CD1	ILE	201	-9.845	62.339	22.914
1662	C	ILE	201	-10.246	66.740	25.359
1663	O	ILE	201	-9.065	66.659	25.705
1664	N	PRO	202	-11.199	67.254	26.123
1665	CA	PRO	202	-11.264	68.709	26.425
1666	CB	PRO	202	-12.547	68.886	27.179
1667	CG	PRO	202	-13.369	67.615	27.069
1668	CD	PRO	202	-12.547	66.681	26.203
1669	C	PRO	202	-10.116	69.368	27.205
1670	O	PRO	202	-10.119	70.594	27.344
1671	N	GLU	203	-9.144	68.616	27.689
1673	CA	GLU	203	-7.980	69.248	28.305
1674	CB	GLU	203	-7.541	68.427	29.510
1675	CG	GLU	203	-8.638	68.361	30.568
1676	CD	GLU	203	-8.914	69.745	31.154
1677	OE1	GLU	203	-7.992	70.309	31.728
1678	OE2	GLU	203	-10.080	70.111	31.188
1679	C	GLU	203	-6.840	69.357	27.292
1680	O	GLU	203	-5.879	70.098	27.524
1681	N	SER	204	-6.958	68.635	26.186
1683	CA	SER	204	-5.957	68.708	25.112
1684	CB	SER	204	-4.875	67.658	25.356
1685	OG	SER	204	-4.087	68.080	26.463
1686	C	SER	204	-6.560	68.499	23.722
1687	O	SER	204	-7.566	67.800	23.537
1688	N	HIS	205	-5.935	69.132	22.745
1690	CA	HIS	205	-6.337	68.947	21.346
1691	CB	HIS	205	-5.946	70.170	20.526
1692	CG	HIS	205	-6.757	71.416	20.809
1693	ND1	HIS	205	-7.917	71.758	20.219
1695	CE1	HIS	205	-8.346	72.932	20.723
1696	NE2	HIS	205	-7.441	73.337	21.642
1697	CD2	HIS	205	-6.454	72.414	21.706
1698	C	HIS	205	-5.649	67.724	20.760
1699	O	HIS	205	-4.417	67.681	20.650
1700	N	PHE	206	-6.445	66.735	20.398
1702	CA	PHE	206	-5.893	65.503	19.830
1703	CB	PHE	206	-6.668	64.291	20.349
1704	CG	PHE	206	-6.362	63.842	21.780
1705	CD1	PHE	206	-5.799	62.589	21.988
1706	CE1	PHE	206	-5.520	62.156	23.278
1707	CZ	PHE	206	-5.809	62.973	24.364
1708	CE2	PHE	206	-6.379	64.222	24.159
1709	CD2	PHE	206	-6.659	64.653	22.869
1710	C	PHE	206	-5.931	65.515	18.306
1711	O	PHE	206	-6.837	66.076	17.678
1712	N	LEU	207	-4.886	64.954	17.730
1714	CA	LEU	207	-4.811	64.736	16.283
1715	CB	LEU	207	-3.694	65.595	15.695

1716	CG	LEU	207	-3.473	65.318	14.206
1717	CD1	LEU	207	-4.703	65.670	13.380
1718	CD2	LEU	207	-2.256	66.066	13.678
1719	C	LEU	207	-4.496	63.274	16.009
1720	O	LEU	207	-3.339	62.857	16.142
1721	N	ARG	208	-5.513	62.488	15.709
1723	CA	ARG	208	-5.245	61.105	15.342
1724	CB	ARG	208	-6.391	60.218	15.792
1725	CG	ARG	208	-6.334	59.973	17.292
1726	CD	ARG	208	-7.433	59.012	17.719
1727	NE	ARG	208	-7.094	58.362	18.993
1728	CZ	ARG	208	-7.477	57.116	19.280
1729	NH1	ARG	208	-7.020	56.515	20.381
1730	NH2	ARG	208	-8.225	56.435	18.408
1731	C	ARG	208	-4.979	60.985	13.847
1732	O	ARG	208	-5.726	61.482	12.991
1733	N	VAL	209	-3.809	60.437	13.581
1735	CA	VAL	209	-3.318	60.229	12.222
1736	CB	VAL	209	-1.807	60.448	12.257
1737	CG1	VAL	209	-1.179	60.279	10.881
1738	CG2	VAL	209	-1.470	61.820	12.826
1739	C	VAL	209	-3.628	58.806	11.779
1740	O	VAL	209	-3.208	57.841	12.430
1741	N	PRO	210	-4.391	58.682	10.704
1742	CA	PRO	210	-4.766	57.368	10.164
1743	CB	PRO	210	-5.846	57.657	9.167
1744	CG	PRO	210	-5.951	59.161	8.962
1745	CD	PRO	210	-4.969	59.788	9.937
1746	C	PRO	210	-3.598	56.647	9.489
1747	O	PRO	210	-3.458	56.678	8.259
1748	N	VAL	211	-2.783	55.981	10.289
1750	CA	VAL	211	-1.663	55.217	9.746
1751	CB	VAL	211	-0.511	55.251	10.742
1752	CG1	VAL	211	0.701	54.528	10.172
1753	CG2	VAL	211	-0.144	56.683	11.108
1754	C	VAL	211	-2.077	53.773	9.505
1755	O	VAL	211	-2.116	52.964	10.437
1756	N	ASN	212	-2.475	53.477	8.281
1758	CA	ASN	212	-2.814	52.095	7.945
1759	CB	ASN	212	-3.391	52.062	6.531
1760	CG	ASN	212	-3.885	50.667	6.165
1761	OD1	ASN	212	-3.091	49.803	5.778
1762	ND2	ASN	212	-5.169	50.438	6.371
1765	C	ASN	212	-1.548	51.245	8.086
1766	O	ASN	212	-0.436	51.712	7.825
1767	N	ASP	213	-1.721	50.020	8.552
1769	CA	ASP	213	-0.585	49.153	8.890
1770	CB	ASP	213	-1.025	48.214	10.012
1771	CG	ASP	213	-2.251	47.397	9.602
1772	OD1	ASP	213	-3.355	47.845	9.884
1773	OD2	ASP	213	-2.058	46.299	9.099
1774	C	ASP	213	-0.023	48.339	7.717
1775	O	ASP	213	0.936	47.584	7.915
1776	N	SER	214	-0.602	48.459	6.532
1778	CA	SER	214	-0.058	47.751	5.366
1779	CB	SER	214	-1.032	47.848	4.198
1780	OG	SER	214	-1.051	49.200	3.758
1781	C	SER	214	1.271	48.364	4.947
1782	O	SER	214	1.475	49.577	5.070
1783	N	PHE	215	2.070	47.566	4.259
1785	CA	PHE	215	3.412	47.996	3.831
1786	CB	PHE	215	4.265	46.755	3.594
1787	CG	PHE	215	4.533	45.953	4.865
1788	CD1	PHE	215	5.122	46.572	5.961
1789	CE1	PHE	215	5.363	45.848	7.121

1790	CZ	PHE	215	5.017	44.505	7.186
1791	CE2	PHE	215	4.432	43.885	6.089
1792	CD2	PHE	215	4.190	44.609	4.928
1793	C	PHE	215	3.432	48.889	2.583
1794	O	PHE	215	4.509	49.209	2.072
1795	N	CYS	216	2.264	49.299	2.113
1797	CA	CYS	216	2.173	50.207	0.970
1798	CB	CYS	216	1.009	49.750	0.098
1799	SG	CYS	216	1.098	48.041	-0.484
1800	C	CYS	216	1.939	51.654	1.414
1801	O	CYS	216	1.796	52.544	0.568
1802	N	GLU	217	1.881	51.886	2.717
1804	CA	GLU	217	1.550	53.228	3.222
1805	CB	GLU	217	1.106	53.114	4.672
1806	CG	GLU	217	-0.102	52.197	4.791
1807	CD	GLU	217	-1.242	52.682	3.905
1808	OE1	GLU	217	-1.800	53.726	4.218
1809	OE2	GLU	217	-1.568	51.975	2.962
1810	C	GLU	217	2.691	54.239	3.122
1811	O	GLU	217	3.853	53.964	3.449
1812	N	LYS	218	2.313	55.425	2.680
1814	CA	LYS	218	3.241	56.553	2.604
1815	CB	LYS	218	3.047	57.226	1.251
1816	CG	LYS	218	4.097	58.293	0.979
1817	CD	LYS	218	3.893	58.903	-0.401
1818	CE	LYS	218	4.921	59.989	-0.685
1819	NZ	LYS	218	4.708	60.575	-2.016
1820	C	LYS	218	2.951	57.524	3.747
1821	O	LYS	218	1.867	58.112	3.832
1822	N	ILE	219	3.941	57.698	4.604
1824	CA	ILE	219	3.795	58.509	5.814
1825	CB	ILE	219	4.689	57.887	6.889
1826	CG2	ILE	219	4.646	58.672	8.196
1827	CG1	ILE	219	4.278	56.442	7.150
1828	CD1	ILE	219	2.874	56.363	7.741
1829	C	ILE	219	4.179	59.962	5.549
1830	O	ILE	219	3.709	60.860	6.256
1831	N	LEU	220	4.807	60.203	4.411
1833	CA	LEU	220	5.187	61.570	4.006
1834	CB	LEU	220	5.902	61.485	2.664
1835	CG	LEU	220	7.197	60.693	2.812
1836	CD1	LEU	220	7.880	60.476	1.469
1837	CD2	LEU	220	8.152	61.375	3.786
1838	C	LEU	220	4.054	62.627	3.972
1839	O	LEU	220	4.258	63.658	4.625
1840	N	PRO	221	2.870	62.399	3.400
1841	CA	PRO	221	1.821	63.428	3.514
1842	CB	PRO	221	0.704	62.962	2.631
1843	CG	PRO	221	1.033	61.587	2.075
1844	CD	PRO	221	2.409	61.245	2.614
1845	C	PRO	221	1.313	63.659	4.948
1846	O	PRO	221	1.090	64.820	5.327
1847	N	TRP	222	1.408	62.644	5.796
1849	CA	TRP	222	1.005	62.794	7.195
1850	CB	TRP	222	0.689	61.429	7.794
1851	CG	TRP	222	-0.579	60.738	7.326
1852	CD1	TRP	222	-0.798	59.377	7.365
1853	NE1	TRP	222	-2.052	59.126	6.897
1855	CE2	TRP	222	-2.671	60.262	6.545
1856	CZ2	TRP	222	-3.934	60.525	6.025
1857	CH2	TRP	222	-4.315	61.827	5.753
1858	CZ3	TRP	222	-3.442	62.886	5.998
1859	CE3	TRP	222	-2.173	62.631	6.516
1860	CD2	TRP	222	-1.789	61.334	6.785
1861	C	TRP	222	2.102	63.453	8.022

1862	O	TRP	222	1.792	64.136	9.003
1863	N	LEU	223	3.320	63.447	7.503
1865	CA	LEU	223	4.414	64.182	8.136
1866	CB	LEU	223	5.751	63.687	7.598
1867	CG	LEU	223	6.030	62.250	8.017
1868	CD1	LEU	223	7.328	61.744	7.398
1869	CD2	LEU	223	6.080	62.130	9.534
1870	C	LEU	223	4.287	65.670	7.857
1871	O	LEU	223	4.537	66.471	8.762
1872	N	ASP	224	3.635	66.014	6.760
1874	CA	ASP	224	3.373	67.424	6.462
1875	CB	ASP	224	2.833	67.532	5.039
1876	CG	ASP	224	3.803	66.906	4.037
1877	OD1	ASP	224	4.995	67.150	4.166
1878	OD2	ASP	224	3.324	66.265	3.110
1879	C	ASP	224	2.341	67.975	7.445
1880	O	ASP	224	2.650	68.910	8.200
1881	N	LYS	225	1.297	67.188	7.662
1883	CA	LYS	225	0.232	67.576	8.595
1884	CB	LYS	225	-0.901	66.566	8.460
1885	CG	LYS	225	-2.020	66.846	9.457
1886	CD	LYS	225	-3.065	65.735	9.450
1887	CE	LYS	225	-2.455	64.393	9.841
1888	NZ	LYS	225	-3.481	63.338	9.885
1889	C	LYS	225	0.711	67.574	10.045
1890	O	LYS	225	0.487	68.556	10.768
1891	N	SER	226	1.576	66.630	10.373
1893	CA	SER	226	2.082	66.521	11.739
1894	CB	SER	226	2.653	65.123	11.947
1895	OG	SER	226	3.777	64.952	11.096
1896	C	SER	226	3.139	67.575	12.064
1897	O	SER	226	3.093	68.111	13.175
1898	N	VAL	227	3.843	68.085	11.064
1900	CA	VAL	227	4.790	69.176	11.312
1901	CB	VAL	227	5.781	69.264	10.156
1902	CG1	VAL	227	6.560	70.574	10.189
1903	CG2	VAL	227	6.732	68.074	10.160
1904	C	VAL	227	4.050	70.497	11.469
1905	O	VAL	227	4.399	71.285	12.357
1906	N	ASP	228	2.872	70.574	10.870
1908	CA	ASP	228	2.023	71.750	11.050
1909	CB	ASP	228	0.871	71.685	10.049
1910	CG	ASP	228	1.379	71.634	8.610
1911	OD1	ASP	228	0.674	71.059	7.788
1912	OD2	ASP	228	2.371	72.293	8.328
1913	C	ASP	228	1.451	71.778	12.466
1914	O	ASP	228	1.635	72.777	13.174
1915	N	PHE	229	1.066	70.611	12.959
1917	CA	PHE	229	0.464	70.509	14.295
1918	CB	PHE	229	-0.196	69.139	14.388
1919	CG	PHE	229	-1.042	68.891	15.635
1920	CD1	PHE	229	-2.321	69.426	15.714
1921	CE1	PHE	229	-3.105	69.190	16.836
1922	CZ	PHE	229	-2.610	68.419	17.879
1923	CE2	PHE	229	-1.331	67.886	17.802
1924	CD2	PHE	229	-0.546	68.122	16.680
1925	C	PHE	229	1.497	70.672	15.411
1926	O	PHE	229	1.258	71.433	16.360
1927	N	ILE	230	2.706	70.191	15.170
1929	CA	ILE	230	3.773	70.331	16.162
1930	CB	ILE	230	4.883	69.334	15.845
1931	CG2	ILE	230	6.064	69.525	16.786
1932	CG1	ILE	230	4.393	67.897	15.934
1933	CD1	ILE	230	5.503	66.930	15.540
1934	C	ILE	230	4.354	71.741	16.165

1935	O	ILE	230	4.669	72.265	17.240
1936	N	GLU	231	4.253	72.435	15.045
1938	CA	GLU	231	4.761	73.803	14.992
1939	CB	GLU	231	5.053	74.155	13.540
1940	CG	GLU	231	5.797	75.477	13.419
1941	CD	GLU	231	6.190	75.694	11.963
1942	OE1	GLU	231	7.262	75.238	11.590
1943	OE2	GLU	231	5.381	76.247	11.231
1944	C	GLU	231	3.760	74.781	15.593
1945	O	GLU	231	4.174	75.746	16.248
1946	N	LYS	232	2.492	74.403	15.605
1948	CA	LYS	232	1.496	75.223	16.293
1949	CB	LYS	232	0.103	74.842	15.807
1950	CG	LYS	232	-0.073	75.177	14.330
1951	CD	LYS	232	-1.464	74.794	13.839
1952	CE	LYS	232	-1.738	73.313	14.067
1953	NZ	LYS	232	-3.065	72.927	13.561
1954	C	LYS	232	1.594	75.037	17.802
1955	O	LYS	232	1.614	76.039	18.526
1956	N	ALA	233	1.968	73.842	18.232
1958	CA	ALA	233	2.162	73.599	19.666
1959	CB	ALA	233	2.174	72.096	19.894
1960	C	ALA	233	3.471	74.183	20.189
1961	O	ALA	233	3.523	74.671	21.328
1962	N	LYS	234	4.449	74.311	19.308
1964	CA	LYS	234	5.730	74.895	19.695
1965	CB	LYS	234	6.798	74.373	18.739
1966	CG	LYS	234	8.196	74.824	19.143
1967	CD	LYS	234	9.262	74.205	18.247
1968	CE	LYS	234	10.664	74.616	18.684
1969	NZ	LYS	234	11.685	74.023	17.805
1970	C	LYS	234	5.698	76.421	19.680
1971	O	LYS	234	6.348	77.047	20.526
1972	N	ALA	235	4.821	76.998	18.875
1974	CA	ALA	235	4.715	78.460	18.830
1975	CB	ALA	235	4.370	78.881	17.406
1976	C	ALA	235	3.665	79.004	19.794
1977	O	ALA	235	3.742	80.169	20.204
1978	N	SER	236	2.745	78.152	20.212
1980	CA	SER	236	1.736	78.568	21.189
1981	CB	SER	236	0.418	77.878	20.862
1982	OG	SER	236	0.053	78.240	19.537
1983	C	SER	236	2.143	78.213	22.613
1984	O	SER	236	1.558	78.748	23.563
1985	N	ASN	237	3.216	77.445	22.738
1987	CA	ASN	237	3.701	76.962	24.037
1988	CB	ASN	237	4.146	78.125	24.922
1989	CG	ASN	237	5.345	78.825	24.288
1990	OD1	ASN	237	6.427	78.236	24.164
1991	ND2	ASN	237	5.136	80.064	23.878
1994	C	ASN	237	2.629	76.119	24.710
1995	O	ASN	237	1.961	76.542	25.662
1996	N	GLY	238	2.451	74.938	24.145
1998	CA	GLY	238	1.461	73.974	24.628
1999	C	GLY	238	1.837	72.589	24.119
2000	O	GLY	238	0.995	71.895	23.529
2001	N	CYS	239	2.982	72.139	24.612
2003	CA	CYS	239	3.725	70.941	24.168
2004	CB	CYS	239	4.387	70.323	25.393
2005	SG	CYS	239	5.410	71.424	26.398
2006	C	CYS	239	2.907	69.848	23.494
2007	O	CYS	239	1.839	69.447	23.977
2008	N	VAL	240	3.415	69.384	22.368
2010	CA	VAL	240	2.763	68.277	21.673

2011	CB	VAL	240	2.771	68.557	20.173
2012	CG1	VAL	240	4.169	68.889	19.679
2013	CG2	VAL	240	2.162	67.419	19.362
2014	C	VAL	240	3.443	66.949	21.995
2015	O	VAL	240	4.670	66.816	21.910
2016	N	LEU	241	2.652	66.024	22.507
2018	CA	LEU	241	3.128	64.656	22.723
2019	CB	LEU	241	2.402	64.062	23.927
2020	CG	LEU	241	2.804	62.611	24.186
2021	CD1	LEU	241	4.297	62.483	24.460
2022	CD2	LEU	241	2.008	62.020	25.342
2023	C	LEU	241	2.830	63.820	21.484
2024	O	LEU	241	1.660	63.604	21.150
2025	N	VAL	242	3.871	63.411	20.782
2027	CA	VAL	242	3.692	62.559	19.601
2028	CB	VAL	242	4.743	62.918	18.560
2029	CG1	VAL	242	4.575	62.071	17.303
2030	CG2	VAL	242	4.664	64.399	18.214
2031	C	VAL	242	3.825	61.097	20.009
2032	O	VAL	242	4.932	60.549	20.059
2033	N	HIS	243	2.688	60.475	20.264
2035	CA	HIS	243	2.668	59.131	20.844
2036	CB	HIS	243	1.799	59.180	22.099
2037	CG	HIS	243	1.992	58.018	23.055
2038	ND1	HIS	243	1.427	56.797	22.981
2040	CE1	HIS	243	1.853	56.044	24.014
2041	NE2	HIS	243	2.686	56.804	24.757
2042	CD2	HIS	243	2.782	58.023	24.180
2043	C	HIS	243	2.125	58.080	19.878
2044	O	HIS	243	1.027	58.217	19.313
2045	N	CYS	244	2.876	57.004	19.731
2047	CA	CYS	244	2.405	55.873	18.927
2048	CB	CYS	244	3.325	55.672	17.734
2049	SG	CYS	244	2.828	54.350	16.608
2050	C	CYS	244	2.344	54.595	19.769
2051	O	CYS	244	3.374	54.023	20.133
2052	N	LEU	245	1.138	54.053	19.864
2054	CA	LEU	245	0.892	52.873	20.711
2055	CB	LEU	245	−0.610	52.805	20.966
2056	CG	LEU	245	−1.097	53.960	21.831
2057	CD1	LEU	245	−2.605	54.149	21.705
2058	CD2	LEU	245	−0.690	53.751	23.285
2059	C	LEU	245	1.322	51.573	20.043
2060	O	LEU	245	1.554	50.565	20.724
2061	N	ALA	246	1.562	51.635	18.742
2063	CA	ALA	246	1.991	50.460	17.991
2064	CB	ALA	246	1.425	50.559	16.582
2065	C	ALA	246	3.511	50.340	17.913
2066	O	ALA	246	4.021	49.300	17.484
2067	N	GLY	247	4.218	51.351	18.387
2069	CA	GLY	247	5.676	51.309	18.318
2070	C	GLY	247	6.289	52.696	18.244
2071	O	GLY	247	5.753	53.597	17.584
2072	N	ILE	248	7.541	52.754	18.667
2074	CA	ILE	248	8.309	54.008	18.678
2075	CB	ILE	248	9.544	53.780	19.556
2076	CG2	ILE	248	10.278	52.506	19.154
2077	CG1	ILE	248	10.506	54.965	19.565
2078	CD1	ILE	248	9.877	56.213	20.175
2079	C	ILE	248	8.726	54.464	17.273
2080	O	ILE	248	8.894	55.670	17.066
2081	N	SER	249	8.548	53.599	16.286
2083	CA	SER	249	8.948	53.904	14.914
2084	CB	SER	249	8.702	52.668	14.063

2085	OG	SER	249	9.535	51.626	14.547
2086	C	SER	249	8.172	55.074	14.323
2087	O	SER	249	8.802	56.077	13.979
2088	N	ARG	250	6.862	55.093	14.508
2090	CA	ARG	250	6.064	56.145	13.870
2091	CB	ARG	250	4.629	55.657	13.752
2092	CG	ARG	250	4.576	54.344	12.985
2093	CD	ARG	250	3.153	53.813	12.894
2094	NE	ARG	250	3.111	52.544	12.152
2095	CZ	ARG	250	2.123	51.662	12.300
2096	NH1	ARG	250	1.149	51.902	13.177
2097	NH2	ARG	250	2.119	50.533	11.588
2098	C	ARG	250	6.103	57.457	14.646
2099	O	ARG	250	6.185	58.525	14.025
2100	N	SER	251	6.352	57.371	15.943
2102	CA	SER	251	6.427	58.595	16.746
2103	CB	SER	251	6.123	58.278	18.210
2104	OG	SER	251	7.062	57.334	18.708
2105	C	SER	251	7.800	59.249	16.599
2106	O	SER	251	7.883	60.478	16.465
2107	N	ALA	252	8.798	58.429	16.309
2109	CA	ALA	252	10.142	58.935	16.056
2110	CB	ALA	252	11.137	57.805	16.273
2111	C	ALA	252	10.268	59.440	14.629
2112	O	ALA	252	10.911	60.471	14.414
2113	N	THR	253	9.453	58.905	13.736
2115	CA	THR	253	9.440	59.380	12.352
2116	CB	THR	253	8.625	58.406	11.508
2117	OG1	THR	253	9.334	57.178	11.471
2118	CG2	THR	253	8.463	58.891	10.072
2119	C	THR	253	8.825	60.768	12.261
2120	O	THR	253	9.421	61.652	11.633
2121	N	ILE	254	7.834	61.030	13.097
2123	CA	ILE	254	7.224	62.358	13.106
2124	CB	ILE	254	5.853	62.247	13.757
2125	CG2	ILE	254	5.221	63.621	13.928
2126	CG1	ILE	254	4.952	61.341	12.926
2127	CD1	ILE	254	3.547	61.268	13.504
2128	C	ILE	254	8.083	63.382	13.844
2129	O	ILE	254	8.256	64.497	13.334
2130	N	ALA	255	8.826	62.936	14.845
2132	CA	ALA	255	9.707	63.860	15.567
2133	CB	ALA	255	10.123	63.216	16.884
2134	C	ALA	255	10.947	64.212	14.747
2135	O	ALA	255	11.255	65.401	14.590
2136	N	ILE	256	11.461	63.238	14.014
2138	CA	ILE	256	12.631	63.468	13.167
2139	CB	ILE	256	13.209	62.118	12.759
2140	CG2	ILE	256	14.277	62.283	11.689
2141	CG1	ILE	256	13.786	61.378	13.958
2142	CD1	ILE	256	14.249	59.983	13.557
2143	C	ILE	256	12.267	64.267	11.923
2144	O	ILE	256	12.977	65.232	11.616
2145	N	ALA	257	11.057	64.080	11.417
2147	CA	ALA	257	10.613	64.850	10.253
2148	CB	ALA	257	9.383	64.182	9.656
2149	C	ALA	257	10.271	66.287	10.625
2150	O	ALA	257	10.563	67.203	9.842
2151	N	TYR	258	9.902	66.504	11.877
2153	CA	TYR	258	9.688	67.871	12.334
2154	CB	TYR	258	8.931	67.890	13.654
2155	CG	TYR	258	8.683	69.315	14.140
2156	CD1	TYR	258	7.806	70.130	13.437

2157	CE1	TYR	258	7.576	71.432	13.860
2158	CZ	TYR	258	8.229	71.917	14.984
2159	OH	TYR	258	7.935	73.179	15.447
2160	CE2	TYR	258	9.120	71.111	15.680
2161	CD2	TYR	258	9.351	69.809	15.254
2162	C	TYR	258	11.014	68.590	12.517
2163	O	TYR	258	11.150	69.697	11.992
2164	N	ILE	259	12.039	67.889	12.974
2166	CA	ILE	259	13.350	68.527	13.150
2167	CB	ILE	259	14.226	67.598	13.982
2168	CG2	ILE	259	15.612	68.193	14.181
2169	CG1	ILE	259	13.593	67.313	15.337
2170	CD1	ILE	259	14.455	66.354	16.149
2171	C	ILE	259	14.024	68.802	11.804
2172	O	ILE	259	14.536	69.912	11.586
2173	N	MET	260	13.763	67.933	10.841
2175	CA	MET	260	14.296	68.114	9.490
2176	CB	MET	260	14.010	66.853	8.683
2177	CG	MET	260	14.786	65.655	9.213
2178	SD	MET	260	14.376	64.077	8.439
2179	CE	MET	260	14.817	64.490	6.740
2180	C	MET	260	13.669	69.305	8.776
2181	O	MET	260	14.412	70.145	8.258
2182	N	LYS	261	12.377	69.514	8.963
2184	CA	LYS	261	11.704	70.625	8.281
2185	CB	LYS	261	10.258	70.188	8.068
2186	CG	LYS	261	9.447	71.160	7.220
2187	CD	LYS	261	8.056	70.592	6.960
2188	CE	LYS	261	7.168	71.552	6.179
2189	NZ	LYS	261	5.823	70.979	5.996
2190	C	LYS	261	11.759	71.942	9.068
2191	O	LYS	261	11.736	73.020	8.463
2192	N	ARG	262	12.016	71.854	10.362
2194	CA	ARG	262	12.046	73.043	11.222
2195	CB	ARG	262	11.654	72.575	12.623
2196	CG	ARG	262	11.618	73.676	13.676
2197	CD	ARG	262	10.536	74.711	13.393
2198	NE	ARG	262	10.381	75.612	14.546
2199	CZ	ARG	262	10.979	76.801	14.652
2200	NH1	ARG	262	11.729	77.267	13.651
2201	NH2	ARG	262	10.793	77.542	15.747
2202	C	ARG	262	13.424	73.698	11.278
2203	O	ARG	262	13.521	74.929	11.349
2204	N	MET	263	14.473	72.899	11.192
2206	CA	MET	263	15.819	73.469	11.292
2207	CB	MET	263	16.469	72.887	12.542
2208	CG	MET	263	17.636	73.737	13.033
2209	SD	MET	263	17.219	75.450	13.433
2210	CE	MET	263	15.941	75.154	14.678
2211	C	MET	263	16.657	73.189	10.043
2212	O	MET	263	17.829	73.583	9.971
2213	N	ASP	264	16.027	72.567	9.057
2215	CA	ASP	264	16.683	72.159	7.803
2216	CB	ASP	264	17.184	73.378	7.033
2217	CG	ASP	264	17.608	72.969	5.626
2218	OD1	ASP	264	16.730	72.867	4.781
2219	OD2	ASP	264	18.798	72.781	5.413
2220	C	ASP	264	17.817	71.187	8.110
2221	O	ASP	264	19.007	71.511	8.005
2222	N	MET	265	17.422	70.008	8.554
2224	CA	MET	265	18.393	68.987	8.964
2225	CB	MET	265	18.257	68.747	10.465
2226	CG	MET	265	18.659	69.991	11.252
2227	SD	MET	265	18.493	69.900	13.049
2228	CE	MET	265	19.643	68.553	13.395

2229	C	MET	265	18.210	67.675	8.211
2230	O	MET	265	17.121	67.342	7.729
2231	N	SER	266	19.305	66.946	8.097
2233	CA	SER	266	19.275	65.618	7.480
2234	CB	SER	266	20.700	65.160	7.195
2235	OG	SER	266	21.287	64.788	8.437
2236	C	SER	266	18.652	64.614	8.435
2237	O	SER	266	18.636	64.840	9.652
2238	N	LEU	267	18.352	63.437	7.910
2240	CA	LEU	267	17.824	62.339	8.726
2241	CB	LEU	267	17.490	61.188	7.778
2242	CG	LEU	267	17.124	59.902	8.513
2243	CD1	LEU	267	15.935	60.100	9.443
2244	CD2	LEU	267	16.846	58.772	7.531
2245	C	LEU	267	18.847	61.879	9.763
2246	O	LEU	267	18.504	61.759	10.946
2247	N	ASP	268	20.114	61.926	9.382
2249	CA	ASP	268	21.202	61.569	10.295
2250	CB	ASP	268	22.526	61.630	9.537
2251	CG	ASP	268	22.457	60.802	8.256
2252	OD1	ASP	268	22.183	61.394	7.220
2253	OD2	ASP	268	22.622	59.595	8.342
2254	C	ASP	268	21.267	62.538	11.466
2255	O	ASP	268	21.062	62.115	12.612
2256	N	GLU	269	21.285	63.832	11.175
2258	CA	GLU	269	21.395	64.837	12.234
2259	CB	GLU	269	21.624	66.181	11.560
2260	CG	GLU	269	22.967	66.232	10.846
2261	CD	GLU	269	22.978	67.413	9.887
2262	OE1	GLU	269	24.047	67.959	9.656
2263	OE2	GLU	269	21.942	67.619	9.266
2264	C	GLU	269	20.146	64.939	13.109
2265	O	GLU	269	20.283	65.064	14.331
2266	N	ALA	270	18.980	64.678	12.544
2268	CA	ALA	270	17.754	64.770	13.334
2269	CB	ALA	270	16.575	64.932	12.387
2270	C	ALA	270	17.557	63.548	14.223
2271	O	ALA	270	17.222	63.718	15.402
2272	N	TYR	271	18.038	62.395	13.783
2274	CA	TYR	271	17.934	61.198	14.621
2275	CB	TYR	271	18.044	59.951	13.750
2276	CG	TYR	271	17.886	58.641	14.520
2277	CD1	TYR	271	16.999	58.562	15.588
2278	CE1	TYR	271	16.866	57.376	16.297
2279	CZ	TYR	271	17.615	56.266	15.930
2280	OH	TYR	271	17.553	55.121	16.695
2281	CE2	TYR	271	18.486	56.333	14.851
2282	CD2	TYR	271	18.619	57.522	14.143
2283	C	TYR	271	19.026	61.187	15.688
2284	O	TYR	271	18.753	60.800	16.832
2285	N	ARG	272	20.141	61.840	15.408
2287	CA	ARG	272	21.185	61.963	16.426
2288	CB	ARG	272	22.523	62.222	15.748
2289	CG	ARG	272	22.978	60.971	15.006
2290	CD	ARG	272	24.355	61.137	14.378
2291	NE	ARG	272	24.332	62.082	13.251
2292	CZ	ARG	272	25.283	62.995	13.050
2293	NH1	ARG	272	26.251	63.159	13.954
2294	NH2	ARG	272	25.226	63.792	11.982
2295	C	ARG	272	20.870	63.054	17.446
2296	O	ARG	272	21.251	62.913	18.614
2297	N	PHE	273	19.981	63.968	17.093
2299	CA	PHE	273	19.504	64.947	18.068
2300	CB	PHE	273	18.958	66.157	17.319

2301	CG	PHE	273	18.551	67.310	18.228
2302	CD1	PHE	273	19.525	68.151	18.749
2303	CE1	PHE	273	19.163	69.201	19.583
2304	CZ	PHE	273	17.826	69.409	19.896
2305	CE2	PHE	273	16.852	68.568	19.375
2306	CD2	PHE	273	17.214	67.519	18.541
2307	C	PHE	273	18.411	64.333	18.942
2308	O	PHE	273	18.388	64.572	20.158
2309	N	VAL	274	17.705	63.357	18.394
2311	CA	VAL	274	16.709	62.636	19.187
2312	CB	VAL	274	15.757	61.882	18.267
2313	CG1	VAL	274	14.789	61.044	19.085
2314	CG2	VAL	274	14.982	62.838	17.371
2315	C	VAL	274	17.376	61.662	20.155
2316	O	VAL	274	17.024	61.682	21.340
2317	N	LYS	275	18.504	61.086	19.759
2319	CA	LYS	275	19.266	60.236	20.687
2320	CB	LYS	275	20.178	59.287	19.921
2321	CG	LYS	275	19.391	58.332	19.034
2322	CD	LYS	275	20.254	57.154	18.596
2323	CE	LYS	275	21.503	57.599	17.842
2324	NZ	LYS	275	21.154	58.252	16.572
2325	C	LYS	275	20.114	61.051	21.663
2326	O	LYS	275	20.486	60.545	22.727
2327	N	GLU	276	20.246	62.339	21.394
2329	CA	GLU	276	20.914	63.252	22.320
2330	CB	GLU	276	21.337	64.477	21.515
2331	CG	GLU	276	22.061	65.526	22.348
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2337	N	LYS	277	18.673	63.516	23.237
2339	CA	LYS	277	17.717	63.755	24.320
2340	CB	LYS	277	16.526	64.542	23.781
2341	CG	LYS	277	16.945	65.900	23.219
2342	CD	LYS	277	17.605	66.783	24.277
2343	CE	LYS	277	16.634	67.198	25.380
2344	NZ	LYS	277	15.588	68.093	24.861
2345	C	LYS	277	17.254	62.431	24.929
2346	O	LYS	277	16.857	62.382	26.099
2347	N	ARG	278	17.358	61.365	24.151
2349	CA	ARG	278	17.092	60.016	24.661
2350	CB	ARG	278	15.598	59.737	24.629
2351	CG	ARG	278	15.286	58.490	25.446
2352	CD	ARG	278	15.671	58.702	26.905
2353	NE	ARG	278	15.521	57.462	27.679
2354	CZ	ARG	278	14.551	57.261	28.575
2355	NH1	ARG	278	13.636	58.207	28.797
2356	NH2	ARG	278	14.497	56.109	29.247
2357	C	ARG	278	17.788	58.953	23.817
2358	O	ARG	278	17.253	58.513	22.791
2359	N	PRO	279	18.865	58.407	24.357
2360	CA	PRO	279	19.695	57.439	23.624
2361	CB	PRO	279	20.985	57.409	24.383
2362	CG	PRO	279	20.810	58.144	25.704
2363	CD	PRO	279	19.413	58.737	25.675
2364	C	PRO	279	19.119	56.017	23.523
2365	O	PRO	279	19.740	55.157	22.892
2366	N	THR	280	17.952	55.772	24.103
2368	CA	THR	280	17.367	54.423	24.084
2369	CB	THR	280	16.712	54.130	25.429
2370	OG1	THR	280	15.545	54.930	25.544
2371	CG2	THR	280	17.641	54.431	26.600

2372	C	THR	280	16.317	54.248	22.985
2373	O	THR	280	15.642	53.212	22.948
2374	N	ILE	281	16.116	55.264	22.160
2376	CA	ILE	281	15.115	55.153	21.093
2377	CB	ILE	281	14.813	56.551	20.551
2378	CG2	ILE	281	16.083	57.286	20.142
2379	CG1	ILE	281	13.837	56.482	19.386
2380	CD1	ILE	281	13.684	57.828	18.700
2381	C	ILE	281	15.584	54.230	19.963
2382	O	ILE	281	16.686	54.379	19.424
2383	N	SER	282	14.748	53.255	19.639
2385	CA	SER	282	15.037	52.375	18.497
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2387	OG	SER	282	14.601	50.550	19.986
2388	C	SER	282	13.826	52.177	17.575
2389	O	SER	282	13.052	51.226	17.737
2390	N	PRO	283	13.662	53.083	16.622
2391	CA	PRO	283	12.697	52.888	15.538
2392	CB	PRO	283	12.593	54.226	14.873
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2411	CB	PHE	285	15.557	49.993	9.015
2412	CG	PHE	285	15.106	48.601	8.557
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2414	CE1	PHE	285	14.370	47.127	6.801
2415	CZ	PHE	285	14.299	46.079	7.709
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2417	CD2	PHE	285	15.051	47.546	9.461
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2439	CE2	PHE	287	7.331	52.962	10.810
2440	CD2	PHE	287	8.523	53.614	10.524
2441	C	PHE	287	11.771	55.518	7.457
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2452	N	GLY	289	13.636	55.116	4.862
2454	CA	GLY	289	13.570	55.303	3.409
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2493	N	TYR	294	12.072	62.569	2.144
2495	CA	TYR	294	11.563	63.800	2.760
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2497	CG	TYR	294	10.455	64.529	5.006
2498	CD1	TYR	294	11.237	65.246	5.903
2499	CE1	TYR	294	10.662	66.235	6.689
2500	CZ	TYR	294	9.304	66.499	6.583
2501	OH	TYR	294	8.709	67.371	7.468
2502	CE2	TYR	294	8.519	65.788	5.685
2503	CD2	TYR	294	9.097	64.800	4.897
2504	C	TYR	294	12.664	64.851	2.866
2505	O	TYR	294	12.406	66.038	2.635
2506	N	GLU	295	13.900	64.378	2.912
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2522	CE	LYS	296	16.437	64.105	-5.350
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2528	CA	LYS	297	12.156	68.219	-0.869
2529	CB	LYS	297	10.726	67.688	-0.879
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2531	CD	LYS	297	10.067	69.352	-2.661
2532	CE	LYS	297	9.246	70.605	-2.941
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2536	N	ILE	298	13.195	70.299	-0.254
2538	CA	ILE	298	13.370	71.527	0.525
2539	CB	ILE	298	14.864	71.718	0.786
2540	CG2	ILE	298	15.137	72.947	1.649
2541	CG1	ILE	298	15.440	70.479	1.463
2542	CD1	ILE	298	16.919	70.658	1.788
2543	C	ILE	298	12.767	72.723	-0.217
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2545	N	LYS	299	11.991	73.501	0.521
2547	CA	LYS	299	11.353	74.724	0.012
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2549	CG	LYS	299	10.135	76.796	0.945
2550	CD	LYS	299	8.667	76.777	0.516
2551	CE	LYS	299	8.426	76.135	-0.845
2552	NZ	LYS	299	6.997	76.161	-1.188
2553	C	LYS	299	12.334	75.698	-0.646
2554	O	LYS	299	13.275	76.187	-0.010

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